23	24	25	56	27	28	53	30	31	32	33	34
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protein - protein database search, using Smith-Waterman algorithm Thu Feb 26 10:17:57 1998; MasPar time 5.85 Seconds 540.098 Million cell updates/sec Tabular output not generated. MPsrch_pp Run on:

>US-08-874-460-2/ (1-149) from US08874460.pep 1099 1 MNLWLLACLVAGFLGAWAPA......NPISSSKRNVSLLISANSGL 149 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

59021 seqs, 21210388 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Mean 42.837; Variance 68.341; scale 0.627 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

3.75e-06	5.67e-06	1.29e-05	6.50e-05	4.70e-04	1.02e-03	1.02e-03	3.23e-03	3.23e-03	4.71e-03	6.86e-03	1.44e - 02	1.44e - 02	2.09e-02	2.09e-02	3.01e-02	6.21e-02	1.27e-01	1.80e-01	1.80e-01	2.56e-01	3.62e-01
EOTAXIN PRECURSOR (EO	MACROPHAGE INFLAMMATO	C10 PROTEIN PRECURSOR	EOTAXIN PRECURSOR (EO	MACROPHAGE INFLAMMATO	MACROPHAGE INFLAMMATO	MONOCYTE CHEMOTACTIC	MACROPHAGE INFLAMMATO	MONOCYTE CHEMOTACTIC	MONOCYTE CHEMOTACTIC	TONSILLAR LYMPHOCYTE	MACROPHAGE INFLAMMATO	WEE1-LIKE PROTEIN KIN	60S RIBOSOMAL PROTEIN	BONE INDUCING PROTEIN	MONOCYTE CHEMOTACTIC	LYMPHOTACTIN PRECURSO	T-CELL SPECIFIC RANTE	MONOCYTE CHEMOTACTIC	PERIPLASMIC GLUCANS B	LYMPHOTACTIN PRECURSO	HYPOTHETICAL 16.7 KD
EOTA_HUMAN	MI1G_MOUSE	C10_MOUSE	EOTA_CAVPO	MI1A_RAT	MI1B_MOUSE	MCP2_BOVIN	MI1A_HUMAN	MCP2_PIG	MCPI_MOUSE	MI10_HUMAN	MITA_MOUSE	WEE1_DROME	RL7_DICDI	BIP_RAT	MCP2_HUMAN	LTN_RAT	SISD_HUMAN	MCPT_HUMAN	MDOH_ECOLI	LIN MOUSE	YAM5_SCHPO
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119	118	116	112	107	105	105	102	102	101	100	86	86	97	97	96	94	95	91	91	90	68
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ALIGNMENTS

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æ	LUSTER A.D.;	-							
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RN	[3]								
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RA	SMITH H., SH.	SHI X., (SONZ	ALO J.A.	GONZALO J.A., NEWMAN W.,	3		Z-RAMOS J.C.,	
Æ	MACKAY C.R.;								
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RA	BARTELS J., SCHLUETER C.,	SCHLUE	LER	C., RICE	RICHTER E.,	NOS	NOSO N., KULKE	KE R.,	
RA	CHRISTOPHERS E., SCHROEDER J.M.;	Ξ., S(CHRO	EDER J.1	f.;				
RL	BIOCHEM. BIO	PHYS. 1	RES.	COMMUN	. 225:104	5-1	051(1996)		
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38	-1 - SUBCELLULAR LOCATION:	LAK LO	ATT	ON: EXT	EXTRACELLULAR	ż			
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CHEMOTAXIS; INFLAMMATORY RESPONSE; SIGNAL
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EMBL; U06435; G459150;
CYTOKINE; CHEMOTAXIS; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
     STITITES
                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     á
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                                                                    SEQUENCE OF 24-96.
STRAINH-HARTLER; TISSUE-LUNG;
MEDLINE; 94157409.
JOSE P.J., GRIFFITHS-JOHNSON D.A., COLLINS P.D., WALSH D.T.,
MOQBEL R., TOTIX N.F., TRUONG O., HSUAN J.J., WILLIAMS T.J.;
J. EXP. MED. 179:881-887(1994).
J. EXP. MED. 179:881-87 THE PRESENCE OF ALLERGENS, THIS PROFEIN
JI FUNCTION: IN RESPONSE THE ACCUMULATION OF EOSINOPHILS, A PROMINENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE OF ALLERGIC INFLAMMATORY REACTIONS.
--- SUBCELLULAR LOCATION: EXTRACELLULAR.
--- TISSUE SPECIFICITY: LONG.
--- PIM: O-GLYCOSYLATED (PROBABLE).
--- SIMILARITY: BELONGS TO THE INTECRINE BETA FAMILY (SMALL CYTOKINE C-C) (CHEMOKINE CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 clllt-vsafsaqvlahpgipsacc--frvtnkkisfqrlksyki-itsskcpqtaivfe 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
MACROPHAGE INFLAMMATORY PROTEIN 1-ALPHA PRECURSOR (MIP-1-ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RATIUS NORVEGICUS (RAI).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 112; DB 3; Length 96; Pred. No. 6.50e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00472; SMALL_CYTOKINES_CC.
EOSINOPHIL; CYTOKINE; CHEMOTAXIS; GLYCOPROTEIN; SIGNAL.
SIGNAL 1 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-LONG EVANS; TISSUE-LUNG;
JONES M.L., SHANLEY T.P., WARD P.A.;
SUBMITTED (FEB-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
WELLS T.C., WILLIAMS T.J., POWER C.A.;
BIOCHEM. BIOPHYS. RES. COMMUN. 205:788-794(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDULNE; 3028003/.
SHI M.M., GODLESKI J.J., PAULAUSKIS J.D.;
BIOCHEM. BIOPHYS. RES. COMMUN. 211:289-295(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DD28C7E5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY. BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EOTAXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 1-kpdkmicadpkkkwvqdakkyld 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | :::|::|| : || || || || || || 67 LPKRHRKVCGNPKSREVQRAMKLLD 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (REL. 34, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10753 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
10.2%;
Best Local Similarity 28.2%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       C-C) (CHEMOKINE CC).
EMBL; U18941; G687656; -.
EMBL; X77603; G602552; -.
HSSP; P13500; 1MCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CD-1; TISSUE=LUNG; MEDLINE; 95298037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23
72
88
88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 24-57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCYA3 OR MIP1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
ID MILA_RAT
DC 01-0CT-199
DT 01-0CT-199
DD 01-0CT-199
DE MACROPHAGE
GN SCTA3 OR K
CO EUTHERIA;
RN 11
RP SEQUENCE F
RX SEQUENCE F
RX SHI M.M.,
RL BIOCHEM: §
RN ELINE; §
RN ELINE; §
RN SCOURCE I
RN SEQUENCE I
RN MEDLINE;
RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
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  RARARA REPARENTE SOLUTION SOLU
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                  MACROPHAGE INFLAMMATORY PROTEIN 1-ALPHA.
BY SIMILARITY.
BY SIMILARITY.
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-1- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES.
-1- SUBUNIT: HOMODIMER (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE INTECRINE BETA FAMILY (SMALL CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN'1990 (REL. 13, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
MACROPHAGE INFLAMMATORY PROTEIN 1-BETA PRECURSOR (MIP-1-BETA) (H400
PROTEIN) (SIS-GAMMA) (ACT2).
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MACROPHAGE INFLAMMATORY PROTEIN 1-BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-DBA/2J; TISSUE-LIVER;
DAUBERSIES P., LEPRETRE F., BAILLEUL B., GROVE M., PRAGNELL I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUS MUSCULUS (MOUSE).
EURARYOTA; META2OA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHERRY B., TEKAMP-OLSON P., GALLEGOS C., BAUER D., DAVATELIS WOLPE S.D., MASIARZ F., COIT D., CERAMI A.;
J. EXP. MED. 168:2251-2259(1988).
                                                                                                                                                              Score 107; DB 6; Length 92;
Pred. No. 4.70e-04;
9; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6; Length 92;
                                                                             A -> T (IN REF. 2).
C -> W (IN REF. 2 AND 3).
F48CF89F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .:
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PROSITE; PS00472; SMALL_CYTOKINES_CC.
CYTOKINE; CHEMOTAXIS; INFLAMMATORY RESPONSE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 89093958.
BROWN K.D., ZURAWSKI S.M., MOSMANN T.R., ZURAWSKI
J. IMMUNOL. 142:679-687(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.

BY SIMILARITY.

A -> P (IN REF. 1).

E -> Q (IN REF. 1).

D -> H (IN REF. 1).

C543B91F CRC32;
                                                                                                                                                                                                                                                  52 etsslcsqpgvif-ltkrnrgicadpketwvqeyitele 89
                                                                                                                                                                                                                                                                     Score 105; DB 6;
Pred. No. 1.02e-03;
                                                                                                                                                                                                                                                                                                                                                                        92 AA.
                                                                                                                                                                                                                                                                                                                                                                          PRT;
23
92
57
73
6
57
10335 MW;
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92
58
74
75
79
88
10168 MW;
                                                                                                                                                                Match 9.7%;
Local Similarity 41.0%;
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                                                                                                                                                                                                        16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-C) (CHEMOKINE CC).
EMBL; M23503; G533245; -.
EMBL; M35590; G199697; -.
EMBL; X62502; G53127; -.
                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; C30552; C30552
PIR; JL0088; JL0088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 89067830.
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revcadpk-kewvgtyiknldrngmrsepttlfktasalrssaplnvkltrkseanastt 130
                                                                              NAKAO M., NOMIYAMA H., SHIMADA K.;
MOL. CELL. BIOL. 10:3646-3658(1990).
--- SIMILARITY: 464.1 AND 464.2 ARE VERY CLOSELY RELATED.
--- SIMILARITY: BELONGS TO THE INTECRINE BETA FAMILY (SMALL CYTOKINE C.).
C-C) (CHEMOKINE CC).
                                                                                                                                                                                                                                                                                                                               01-AUG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TONSILLAR LYMPHOCYTE LD78 BETA PROTEIN PRECURSOR (G0S19-2 PROTEIN)
    14 LGAWAPAVHTQGVFEDCCLAYHYPIGWAVLRRAW--TYRIQEVSGSCNLPAAIFYLPKRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 90287702.
IRVING S.G., ZIPFEL P.F., BALKE J., MCBRIDE O.W., MORTON C.C.,
BURD P.R., SIEBENLIST U., KELLY K.;
NUCLEIC ACIDS RES. 18:3261-3270(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LD78 BETA / GOS19-2 / BY SIMILARITY.
BY SIMILARITY.
21EDDB04 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 etssgcskpsvif-ltkrgrqvcadp-seewvqkyvsdle 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
9.1%; Score 100; DB 6; 1
Best Local Similarity 45.0%; Pred. No. 6.86e-03;
Matches 18; Conservative 8; Mismatches 11.
                                                                                                                                                                                                                                                                                        93 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 91103879.
BLUM S., FORSDYKE R.E., FORSDYKE D.R.;
DNA CELL BIOL. 9:589-602(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00472; SMALL_CYTOKINES_CC.
                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIIA_MOUSE STANDARD; F
P10855; P14096;
01-JUL-1989 (REL. 11, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 AA; 10161 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C-C) (CHEMOKINE CC).
EMBL; X52149; G296666; -.
EMBL; M24110; G182849; -.
EMBL; D90145; G219908; -.
                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                         128 FSNPISSSKRNVS 140
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58
74
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PROSITE; PS00472; SMAI
CYTOKINE; CHEMOTAXIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; B30412; B30412.
PIR; B35673; B35673.
PIR; S10157; S10157.
HSSP; P13236; 1HUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [3]
SEQUENCE FROM N.A.
MEDLINE; 90287155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; B30908; B30908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 (PAT 464.2).
SCYA3L1 OR 464.2.
                                                                                                                                                                                                                                                             LT 11
MI10_HUMAN
P16619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                             131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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ID MI
AC P1
DT 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- INDUCTION: BY PLATELET-DERIVED GROWTH FACTOR.
-!- SIMILARITY: BELONGS TO THE INTECRINE BETA FAMILY (SMALL CYTOKINE CC).
C-C) (CHEMORINE CC).
EMBL; J04467; G387169; -.
EMBL; A30209; A30209.
PIR; A30209; A30209.
PIR; A3061; A30861.
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01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
MONOCYTE CHEMOTACTIC PROTEIN 1 PRECURSOR (MCP-1) (PLATELET-DERIVED SCROWTH FACTOR-INDUCIBLE PROTEIN JE).
SCYAZ OR MCP1 OR JE.
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MEDLINE: 91293127.
WAN DAMME J., DECOCK B., BERTINI R., CONINGS R., LENAERIS J.-P.
PUT W., OPDENAKER G., MANITOVANI A.;
EUR. J. BIOCHEM. 199:223-229(1991).
-1- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES, BUT N
NEUTROPHILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; RODENTIA.
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  MONOCYTE CHEMOTACTIC PROTEIN 2. PYRROLIDONE CARBOXYLIC ACID (BY
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Pred. No. 4.71e-03;
41; Mismatches 52; Indels
                                                                                                                                                            Score 102; DB 6; Length 99;
Pred. No. 3.23e-03;
11; Mismatches 18; Indels
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SEQUENCE FROM N.A.
MEDLINE; 88234501.
ROLLINS B.J., MORRISON E.D., STILES C.D.;
PROC. NATL. ACAD. SCI. U.S.A. 85:3738-3742(1988).
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                                                                 BY SIMILARITY.
BY SIMILARITY.
B7620BCF CRC32;
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BY SIMILARITY.
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BY SIMILARITY.
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SEQUENCE FROM N.A.
MEDLINE; 89093129.
KAWAHARA R.S., DEUEL T.F.;
J. BIOL. CHEM. 264:679-682(1989).
                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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126 PO
16326 MW;
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75
10903 MW;
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9.2%;
Best Local Similarity 23.3%;
Matches 31; Conservative
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Best Local Similarity 34.0%;
Matches 16; Conservative
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148
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35
99 AA;
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P10148;
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                                                                             12 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE; 90370447.

SITUATION: BINDS TO G-RICH STRUCTURES IN 28S RRNA AND IN MRNAS.

IL NUCLEIC ACIDS RES. 18:4695-4701(1990).

PLAYS A REGULATORY ROLE IN THE TRANSLATION APPARATUS; INHIBITS

CELL-FREE TRANSLATION OF MRNAS (BY SIMILARITY).

CHANGE TRANSLATION OF MRNAS (BY SIMILARITY).

CHANGE TRANSLATION OF THE L30P FAMILY OF RIBOSOWAL PROTEINS.

BEMBL; X14909; G7357; --

CHANGE DOUGHOUT.

PROSTITE; PSO0634; RIBOSOWAL_L30.

RIBOSOWAL PROTEIN; RNA-BINDING.

SEQUENCE 246 AA; 27932 MW; 72367CC8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Gaps
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                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-FEMUR;
TAKAO M., HINO J., KANGAWA K., MATSUO H.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-1- SUBUNIT: HOMODIMER OR HETERODIMER (POTENTIAL).
-1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
EMBL; D49494; G699625; -.
SIGNAL; GROWTH FACTOR; CYTOKINE; GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                       ;;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 97; DB 1; Length 476;
Pred. No. 2.09e-02;
22; Mismatches 26; Indels
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BONE INDUCING PROTEIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
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Pred. No. 2.09e-02;
12; Mismatches 22; Indels
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42D22B46 CRC32;
                         STRAIN-AX2;
MEDLINE; 89345108.
SZYMKOWSKI D.E., KELLY B., DEERING R.A.;
NUCLEIC ACIDS RES. 17:5393-5393(1989).
                                                                                                                                                                                                                                                                                                         Query Match 8.8%;
Best Local Similarity 36.8%;
Matches 21; Conservative
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Best Local Similarity 31.7%;
Matches 26; Conservative
[1]
SEQUENCE FROM N.A.
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198 qakdissiikaarrdgelllsa 219 :| :|: | :::|

125 SSK-FSNPISSSKRNVSLLISA 145

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Search completed: Thu Feb 26 10:18:20 1998 Job time: 23 secs.

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Release 2 Copyright	2.1D John F. Collins, Biocomputing Research Unit. c. (c) 1993, 1994, 1995 University of Edinburgh, U.K. Sistribution rights by IntelliGenetics, Inc.
MPsrch_nn n.a.	- n.a. database search, using Smith-Waterman algorithm
Run on: Tabular output not	Thu Feb 26 10:48:37 1998; MasPar time 550.37 Seconds 887.394 Million cell updates/sec t generated.
Title: Description: (Perfect Score: 9 N.A. Sequence: Comp:	1-989) from USO8874460.seq 989 CCGCGGGCATCACCTCCCT
Scoring table: T	TABLE default Gap 6
Nmatch STD: D	Dbase 0; Query 0
Searched: 6	665703 seqs, 246912890 bases x 2
Post-processing: M	Minimum Match 0% Listing first 45 summaries
Database: E	1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8 1:EST1 2:EST1 2:EST1 11:EST1 11:EST3 11:EST4 11:EST5 11:EST6 11:EST6 11:EST6 11:EST6 11:EST7 11:EST7 11:EST7 11:EST7 11:EST6 11:EST6 11:EST7 11:EST1 1

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N73958 407 bp mRNA EST (19-MAR-1995/
2a74fd4.s1 Homo sapiens cDNA clone 298303 3'.
N73958
91231243
EST.
human clone=298303 primer-ml3 -40 forward library-Soares fetal lung
NDHL19W vector-pT7T3D (Pharmacia) with a modified polylinker
                                                                                                                                                                            ## 8.43e-153
## 1.96e-79
## 1.96e-79
## 1.96e-79
## 1.96e-11
## 1.96e-13
                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 183:EST183
188:EST188
193:EST193
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                                                    scale 3.035
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                                                   Variance 3.780;
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SSZ84185
W91616
AA046476
AA035211
H75269
H75269
N95880
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N67550
NATSO
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AA136868
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AA189534
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AA017921
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AA032833
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ACCESSION
NID
KEYWORDS
SOURCE
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COMMENT

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Contact: Wilson RK
WashUrMerck EST Project
WashUrMerck EST Project
WashUrMercsity School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Ema: 314 286 1800
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2830 StG Error: 0.00
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 55.
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AA035211 91507392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 275)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 5.32e-13;
0; Mismatches 10; Indels
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/lab_host="DH10B (ampicillin resistant)"
complement(<1..>172)
139 c 43 g 52 t 2 others
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/clone_lib="Soares retina N2b4HR"
/sex="male"
                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="retina'
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Best Local Similarity 82.8%;
Matches 48; Conservative
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                                                                                                                                                                                                                                FEATURES
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                                                                                                                                                                                                                                                             /strain-"C57B1/6"
/note="Vector: pcDNA1; Site_1: Not1; Site_2: EcoR1; The cDNA library was constructed from poly(A)+ RNA of an adult mouse thymus by oligo-dT primed reverse transcription.
CDNA was selected on gel for size above 800 notleotides after second strand synthesis, then directionally cloned after adaptor ligation and restriction enzyme cleavage into the pcDNA1 vector (Not 1 on polyA side, EcoR 1 on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU46474 172 bp mRNA EST 02-FEB-1997
2f48g09.s1 Soares retina N2D4HR Homo sapiens CDNA clone 380224 3'.
AA046474
91526404
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                                 Genome Structure and Immune Functions
Centre d'Immunologie INSERM/CNRS
Centre d'Immunologie INSERM/CNRS
Tel: 330491269496
Fax: 330491269430
Email: jordan@ciml.univ-mrs.fr
This sequence was determined at HGMP Resource Centre, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 ttttgcctgcctggttgcntctttgttgggggcctggatgccggttgtccatgcccaagg 142
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/clone="MTA.F02.091"
/clone=lib="MTA adult mouse thymus library"
/lab_bost="MC1061 p3"
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Pred. No. 1.96e-79;
0; Mismatches 75;
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70.1%;
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                   Contact: Jordan BR
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DEFINITION ACCESSION

RESULT LOCUS ORGANISM

REFERENCE AUTHORS

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TITLE JOURNAL COMMENT

mRNA BASE COUNT ORIGIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="vector: ZipLox; Site_1: Sall; Site_2: NotI; ds-cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT oligo-
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Tel: 314 286 1810
Fax: 314
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trenskis,E., Materston,R., Williamson,A., Wohldmann,P. and
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Pred. No. 3.78e-11;
0; Mismatches 2; Indels
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                                                                                                                              E-mail: robferlnervm.nerdc.ufl.edu
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                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Gainesville, FL 32611-0695
ph: 904-392-1928, ext. 301
fax: 904-392-4072
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Best Local Similarity 95.0%;
Matches 38; Conservative
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melanocyte
double-stranded cDNA was size selected, ligated to Eco RI address (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of Mormalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 146)
Hilliar,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Theraskis,E., Materston,R., Williamson,A., Wohldmann,P. and
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 135; Length 450; Pred. No. 3.78e-11;
                                                                                                                                                                                                                                                                                                                                                         5 others
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/lab_host="DH10B (ampicillin resistant)"
complement(<1..>450)
1 104 c 121 g 129 t 5 other
                                                                                                                                                                                             /clone="358374"
/clone_lib="Soares fetal heart NbHH19W"
/sex="unknown"
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Homo sapiens cDNA clone 269571 3'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
WashU-Merck EST Project
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Best Local Similarity 76.5%;
Matches 52; Conservative
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Fax: 314 286 1810
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Homo sapiens
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                                                                              Bucaryotes, Metacoa, Chordata; Vertebrata; Gnathostomata; Mammalia; Bucaryotes, Metacoa, Chordata; Vertebrata; Gnathostomata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo., Clark, N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l (bases 1 to 329)
Marra M., Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Marra M., Hiller, L., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and Cloned into the Not I and Eco RI sites of the modified pI7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.
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                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
Hashington University School of Medicine
Hashington University School of Medicine
Had Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
Email: sat@watson.wustl.edu
Force: IMAGE Consortium, LLNL
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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WashD-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
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Pred. No. 3.07e-10;
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Best Local Similarity 81.3%;
Matches 52; Conservative
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/organism="Homo sapiens"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT. Skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA196465 360 bp mRNA EST 22-JAN-1997
zp98h12.s1 Stratagene muscle 937209 Homo sapiens cDNA clone 628295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
WashU-Werck EST Project
WashU-Werck EST Project
WashU-Werck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Ema: 34 286 1810
Email: est@watson wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 123.
Location/Qualifiers
Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:888915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 360) Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, Materston, R., Milliamson, A., Wohldmann, P. and Wilson, E., WashU-Merck EST Project Unpublished (1995)
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                                                                                         Putative full length read
vector to vector length is 353
Seg primer: -28Ml3 rev2 from Amersham.
                                                                                                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                  Location/Qualifiers
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Best Local Similarity 88.5%;
Matches 46; Conservative
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US-08-874-460-1.rstb

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by Intelligenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

Thu Feb 26 10:59:09 1998; MasPar time 301.05 Seconds 926.471 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-874-460-1 (1-989) from US08874460.seq 989 Title:

Description:
Perfect Score:
N.A. Sequence:
Comp:

1 CCGCCGGCCATCAGCTCCCT.
GCCCGCCCGTAGTCGAGGGA.

default TABLE Gap 6 Scoring table:

Query 0 Dbase 0; •• Nmatch STD

397346 segs, 141010104 bases Searched:

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Minimum Match 0% Listing first 45 summaries Post-processing:

EST-C Database:

EST107 2:EST198 3:EST199 4:EST200 5:EST201 6:EST202 7:EST203 8:EST204 9:EST205 10:EST200 11:EST207 12:EST208 13:EST203 8:EST204 9:EST205 10:EST206 11:EST207 12:EST208 13:EST209 14:EST209 14:EST205 10:EST212 17:EST213 18:EST213 18:EST213 17:EST213 18:EST213 18:EST213 18:EST213 22:EST213 23:EST213 24:EST223 25:EST223 24:EST223 25:EST223 24:EST223 24:EST223 24:EST223 24:EST223 24:EST223 24:EST224 24:EST223 24:EST223 24:EST223 24:EST224 24:EST224 24:EST223 24:EST224 24:EST223 24:EST224 24:EST224 24:EST223 24:EST224 24:EST224

Database:

Mean 11.352; Variance 3.381; scale 3.358 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description Pred. No.	7101116 Thymus III 0.00e+00 7101182 Thymus III 0.00e+00 7101182 Thymus III 0.00e+00	101169 Thymus III 2	18.rl Soares mou 3.22e-14	an retal brain cDN 3 8e02.rl Soares mou 3	uman aorta cDNA 5'-e 3 t04e07.rl Soares mou 3	4.rl Soares mou 3 fetal brain cDN 3	rl Soares mou 3	3.rl Soares mou 3 3.rl Barstead m 3	mou 3.43e	5.rl Soares mou 3	7.rl Soares mou 3	1.rl Soares mou 3	1.rl Soares mou 3	fetal brain cDN 3	s.ri soares mou 3 5.si Knowles So	rl Soares mou 3 rta cDNA 5'-e 3	sl Soares ova 3	rl Soares mou 3	<pre>d cDNA lib 3.30e-10 Soares mou 3.30e-10</pre>	NA, partial se ri Soares mou 3	NA, partial se	2b05.s1 Stratagene 3	188g05.sl Stratagene 3.30e	res mou 3.30e-10			EST 18-APR-1997 ens cDNA 5' end.		, aryotes; Metazoa; Chordata; a; Primates; Catarrhini; Hominidae;	chmann, R.D., Fuldne Weinstock, K.G., Brandon, R.C., Man-1 A.D., Earle-Hughes, itchman, J.L., Geo, Hedblom, E., Hink, L., Marmaros, S.M.,
SUMMARIES	AA295814 AA295958	AA295945	AA270684	AA237207	C16161 AA176034	AA260469 C14394	AA270895 AA267728	AA396012 AA241100	AA276953 AA267708	AA221995 AA219890	AA273932 AA259890	AA220092 AA436703	AA268648	C14215	AA445723	AA238809 C16061	AA402661	AA241234		RICC1646B	RICR2825A	AA227123	AA121171 AA440484	AA271476 AA042856	ALIGNMENTS		mRNA Homo sapi		lrial euk Eutheri	Ge,A.R., Fleisc, Kirkness,E.F., Talke,J.A., E, T.R., Cotton, tzhugh,W.M., Fl. L., Hanna,M.C.,
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å Query Match	28.	. m -	i m (•		AA295814 EST101116 AA295814	<u> </u>	Homo sapi Eukaryota Vertebrata	base s,M. C.J. e,O. ton, ton, gera ek,A
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I dases 1 to 274)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bulli, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man Wai, C.
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Flizgerald, L.M., Flitzhugh, W.M., Fritchman, J.L., Geoglagen, N.S.,
Glodek, A., Gnehm, C.L., Hand, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Moreno-Palanques, R.F., McDonald, L.A., Mayven, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shiley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, B.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wilng, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haselline, W.A., Fields, C.,
Intial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TiGR Human Gene
index (http://www.tigr.org/tdb/hgi.hgi.html)
Seq primer: M13 Reverse.
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Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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Pred. No. 9.84e-300;
0; Mismatches 8; Indels
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The Institute for Genomic Research
712 Medical Center Drive, Rockville, MD 20850 USA
721: 3018699056
Fax: 3018699423
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Best Local Similarity 96.7%;
Matches 261; Conservative
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Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.S., Brandon, R.C., Man-Wal, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hadblom, E., Hinkle, P.S.Jr.,
Kelley, J.M., Kelley, J.C., Luiu, L.-I., Marmaros, S.M., Merrick, J.M.
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Bhan, M.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Well, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Francon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of CDNs, sequence
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712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
information related to this EST, please check the TigR Human Gene
Information./www.tigr.org/tdb/hgi/hgi.html)
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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<1..>256
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                                                                                                                                                                            18-APR-1997
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EST101169 Thymus III Homo sapiens cDNA 5' end.
91948290
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Pred. No. 2.47e-266;
0; Mismatches 4;
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Seq primer: M13 Reverse.
Location/Qualifiers
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Contact: Kerlavage, AR
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Best Local Similarity 97.3%;
Matches 249; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 256)
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Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
CO.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
Japan (Tel:*81-886-65-288, Fax:+81-886-37-1035)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    Fujwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y., Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T., Otsuka cDNA project
Unpublished (1996)
2 (bases I to 428)
Fujiwara,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mx18e02.rl Soares mouse NML Mus musculus cDNA clone 680570 5' similar to TR:G215212 G215212 P2, LACZ INSERT FRAMESHIFT MUTATION
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                  Gaps
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                                                                                                                                                                                                                        EST(expressed sequence tag); Human fetal brain.
Homo sapiens fetus brain cDNA to mRNA, clone:056B05.
Homo sapiens
 Length 231;
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              Pred. No. 3.22e-14;
0; Mismatches 9; Indels
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Pred. No. 3.22e-14;
5; Mismatches 20; Indels
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Euman fetal brain cDNA 5'-end GEN-056B05.
C14427
 DB 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
 Score 37;
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/dev_stage="fetus"
/tissue_type="brain"
a 56 c 74 g
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              Best Local Similarity 83.6%;
Matches 46; Conservative
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Best Local Similarity 67.1%;
Matches 51; Conservative
3.78;
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Direct Submission
Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (sites)
Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
Maekawa,H., Nakamura,Y. and Takahashi,E.
Otsuka cDNA project
Unpublished (1996)
2 (bases 1 to 224)
Fujiwara,T.
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                          WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
WashIngton University School of MedicineP
WashIngton University School of MedicineP
WashIngton University School of Medicine Work 1800
Fax: 314 286 1800
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-SEP-1996
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Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                Possible reversed clone: similarity on wrong strand Seq primer: -28ml3 rev2 Er from Amersham High quality sequence stop: 232. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 432;
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EST(expressed sequence tag); Human aorta.
Homo sapiens aorta cDNA to mRNA, clone:234B03.
Homo sapiens
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Pred. No. 3.22e-14;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="680570"
/clone_lib="Soares mouse NML'
/tissue_type="Liver"
/lab_host="DH108"
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Human aorta cDNA 5'-end GEN-234B03.
C16161
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                                                                                                                                            Contact: Marra M/Mouse EST Project
                                                                       The Washu-HHMI Mouse EST Project
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Best Local Similarity 97.4%;
Matches 38; Conservative
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69
                                                                                               Unpublished (1996)
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REFERENCE AUTHORS

KEYWORDS SOURCE

TITLE JOURNAL

REFERENCE

AUTHORS TITLE JOURNAL

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(bases 1 to 413)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA267728 413 bp mRNA EST 21-MAR-1997 mz66e03.rl Soares mouse lymph node NbMLN Mus musculus cDNA clone 718396 5'. AA267728 g1904462
                                   Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
MashIngron University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata,
Vertebrata, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.5%; Score 35; DB 47; Le
Best Local Similarity 94.9%; Pred. No. 3.45e-12;
Matches 37; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    368
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                  Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 353.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                             1..403
/organism="Mus musculus"
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The WashU-HHMI Mouse EST Project
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Unpublished (1996)
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Direct Submission
Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu Submitted, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co., Ltd: 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
                                                                                                                                                                                                                                                                                                                                                                                                                              Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y., Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T., Mackawa,H., Nakamura,Y. and Takahashi,E.
Otsuka cDNA project
Unpublished (1996)
2 (bases 1 to 430)
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/clone="053D02"
/dev_stage="fetus"
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Query Match

Matches

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FEATURES

13

RESULT

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ACCESSION

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KEYWORDS SOURCE

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TITLE

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Gaps

(MI)

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn Run on:

Thu Feb 26 10:19:02 1998; MasPar time 1183.69 Seconds 1186.804 Million cell updates/sec

Tabular output not generated.

>US-08-874-460-1 (1-989) from US08874460.seq 989 Title: Description: Perfect Score: N.A. Sequence:

......... 1 CCGCCGGCCATCAGCTCCCT

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 Nmatch STD 430261 seqs, 710217276 bases x 2 Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

embl-new7 1:BCT 2:FUN 3:GEN 4:HTG1 5:HTG2 6:HTG3 7:HTG4 8:HUM1 9:HUM2 10:HUM3 11:INV1 12:INV2 13:ORG 14:MAM 15:VRT 16:PLN 17:PRO1 18:PRO2 19:ROD 20:SYN 21:UNC 22:VIR

genbanka101 Database:

33.BCT1 24.BCT2 25.BCT3 26.BCT4 27.BCT5 28.BCT6 29.BCT7 30.BCT8 31.BCT9 33.BCT10 33.BCT11 34.BCT12 35.BCT13 36.GEN1 37.GEN2 38.BCT10 33.BCT11 34.BCT12 35.BCT13 36.GEN1 37.GEN2 38.GEN3 49.GEN4 40.GEN5 41.GEN6 42.BCT13 43.BCT13 44.BCT2 35.BCT13 46.BCT4 41.GEN6 44.BCT 44.BCT 44.BCT 44.BCT 44.BCT 44.BCT 44.BCT 44.BCT 45.BCT 48.BCT 48.BCT 49.ENV9 56.INV1 57.INV1 58.INV1 55.INV6 53.INV7 54.INV8 55.INV9 56.INV1 57.INV1 63.WAT1 60.MAM 61.MAM 55.INV9 56.INV1 63.VAT 46.BCT 77.PAT 63.BAT 77.PAT 63.BAT 77.PAT 78.PG 74.PLN1 75.PLN 76.PAT 64.PLN1 76.PLN 77.PLN 77.PAT 86.PN1 84.PLN1 76.PLN 77.PN1 87.PN1 8

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Database:

115:VRL1 116:VRL2 117:VRL3 118:VRL4 119:VRL5 120:VRL6 121:VRL7 122:VRL8 123:VRL9 124:VRL10 125:VRL11 genbank-new7

126:BCT 127:GEN 128:HTG1 129:HTG2 130:INV 131:MAM 132:VRT 133:PHG 134:PLN1 135:PLN2 136:PRI1 137:PRI2 138:ROD 139:SYN 140:UNA 141:VRL

142:part1 143:part2 Database:

Mean 11.647; Variance 10.251; scale 1.136 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

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12-JUN-1993	Chordata; Myomorpha; Muridae;	ie IMP dehydrogenase [Unpublished (1990)]
MUSIMPD 1707 bp mRNA ROD MOUSE IMP dehydrogenase mRNA, complete cds. 4M33934 1M29833 IMP dehydrogenase. Mouse, cDNA to mRNA.	nus mustatus Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus. 1 (bases 1 to 1707)	Tiedeman, A.A. and Smith, J.M. Isolation and sequence of a cDNA encoding mouse IMP dehydrogenase Gene 97, 289-293 (1991) 91153661 Draft entry and computer-readable sequence for [Unpublished (1990)]
RESULT 1 LOCUS DEFINITION ACCESSION NID KEYWORDS SOURCE	REFERENCE	AUTHORS TITLE JOURNAL MEDLINE COMMENT

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COTCEPOODALEKSKREGATINAGMISGIKKIAPITMISCATILERINIKELEGRISTINE
CADDTQOYRITHLENFCEDARAFEALRNDIEALGAGSTYPELPSPSGNSGTAGE
ORPOSTRRRRPPVEWSEAGAGETVIVGOBEOGAHQDSSVAAAGPADEHNAMLOKIT
LGSFKWKVSDGGSILKTFSLFSDIRAANDRAKNFLSFTOTYTCEGMIFTLITISIGL
HGGTLLVAMDALSSATRRGIVSMIQLSNLPSMITHASGSSIGTLVTSPAIQHQICTS
GSBGSILANIGSLYISVANVLCADSAAADELNVRWAWOVSNRPKLSYWTAQHGICTS
GSBGSILANIGSLYISVANVLCADSAAADELNVRWKLSYWTAQHGSTAOGGGF
ESQDLGDLQAIIATGKWSTTSDKNLMEIIVHPTACTVSFKLYWTLDPLWSTREFF
SGSKRYTFVFGASKMFDRGKINVSRVLHVMILDPLWTGNASNSIGFYVVAG
PGKGFKLHQWGGYKSQFAHDVITAAQDFGRSISGSRLCANGFKRWTGNSSNSIGFYVVAG
PGKRRAFKYAVTPRMRTLPPBATSLSMLSQIFVEWRGSLYTITHQGSGSAIQHSYWRIW
YDPNGKTDEREVKFLDSARADELNYSTINENSKELTYTHIVQSGSAIQHSYWRIW
YDPNGKTDEREXVERDLRSGADMELRYSIANGOBFRYNGT
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AWEMVERTPTMSKKQVGPELTVSDPQMYKCIKNMNKNVKILTDRQCTAKLANIVDSA
QELVGSNSTFVEDLAVGAKQIRKFGESLDVFEGSMSAAKTAELIDNTHAAFSGPADGS
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PLFARLVLMYRGFAPLDNSHVIEEDEMDICGHSSEVTYEDPSKFAFTHQHVTRGVGMG
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SRSLGGLLSFYRGLRGYNYVSCREETHHABGFRHWSFRSQRPFPDRYXFABERMYPPLGYV
HLTSKWPRCRLLIDDLSSLMSRYABSSQAQAGEIYEBTFDEDDLFELDGEGETSTR
GLLDLGRRLGGLLLGATKCVRGLHSVIEWPVDVLIKEAEDLGTWLADNKKYVSESTWS
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WGKIPDDKEITTSFADKFHSIGKKGRSITNIIGGFEKITSVCKKWSETLVSWIVSNVSG
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Submitted (16-JUN-1992) Ping Shen, The Scripps Research Institute,
MRC-7, 10666 North Torrey Pines Rd., La Jolla, CA 92037, USA
Location/Qualifiers
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                                                                                                                                                       10-MAY-1995
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Nucleotide sequence and genomic organization of rice tungro
spherical virus
Virology 193 (2), 621-630 (1993)
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                                                                   Length 1779;
                                                                score 37; DB 110; Length 17;
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0; Mismatches 16; Indels
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complete genome; polyprotein.
Rice tungro spherical virus RNA.
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                                                                Query Match 3.7%;
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Matches 53; Conservative
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LOODHOWVAALVILVACAVKERRRWTHPKLHRKSFNALDKLDANTTTAARTSKKMKIL
LAIGASVAVAGVVAVGAVKERRRWTHPKLHRKSFNALDKLDANTTTAARTSKKMKIL
LAIGASVAVAGVVAVGAVILLOKTNLFGSKEDEEIEGEEGTQASGAHESDGIVTQHLK
RDIRRKMYVYTDHHYAEAHEEKDAKRRRSKEDFRKSSTGLESPERABRGWYTYEH
TPLKDALLDESNKVFRRYNASVESARKSKOFVLSQIGDWOKVKATGVIAAR
QLEAGSSLKKIHNLASRRTSSHVMPGLVVHOGGRASKDTVLSQIGDWOKVKATGVIAAR
IKEGVSTLSVKKASVGMLALQKAESQLSFPFTSRAGVDRDLSMTNLIDFHMAGMSCII
ISELGNVFRTFGVLRLCGTYVCMPAHYLDEITSEHTLYFVCPSKITQIQLERHRVCLV
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DSTELTERANSVSPTSYXEANGGIHTISGLKXFVCHOMFCFCGRAIMRADATCFRKIG
MYSGLERNKCMGYAGTILOGHLMQALFTLKFITGLKHIPRGALGAGEBKLPEBSKKQS
LSLEGKGNLGIVGQLTAQLVPTSVTKTICKSMIHGLIGEIKTEPSVLSAWDRRLPFP
                        FERVEXRIFLRFLCMYIDAYMXSQEQVLQGIKTFKMNPFAPEPEFAQAQNGEAAECEI
VEEMOEVOEAPELVK ETAPANDELVEARKIKLAYPGHUDLIROSGGCYIDE
VATAGPEMLSFHELL-PFTGCGHHTRYCDFNIYYNNMCKAVRSGSVHFKYRANQAIKYA
YTHKLHSQCRYSIDPEKLRECNPLDVFVCVLSKYTADDHSFERRCPKKMNVVRMQRPP
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YERIKEEVTSGVKPSIMTMECLKDERRKLAKIYEKPATRTFTILSPEVNILFRQYFGD
FAAMVMSTRREHFSQVGINPESMEWSDLINSLLRVNTKGFAGDYSKFDGIGSPAIYHS
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NYYFWALAWMSTVGSSLLSPQGSCKDFDTYCKIVAYGDDNVVSVHEEFLDVYNLQTVA
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RLNWIRDCPTPVEALEQNIESALHEAAIHGRDYFDDLVRRLNSALTRVMLPPTDISFE
LVKVERDPDVPKNEANPTEGLVFTVLGHDQNCQGDPQFVVKENWDEPFLREVDTEGWR
                                                                                                                                                     VFELKMRPPSDSVVVEDEQGQRIFEWPHLYIFLRYRALEFKDDKGSLTVREDAGADVC
PWNEFLKLPWLDGDQLKSVLPAHLHRWVQARLEQVEIMEENGNYSGEMRNAIAEIKEY
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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CDNA encoding beta-chain of human lymphocyte antigen DR-B.
E00200
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PC C12N15/00,C07C103/52,C07H21/04,C12P19/34,C12P21/02,
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PD 02-JUN-1984
PF 30-JUL-1982 GB 82 8222066, 25-OCT-1982 GB 82
BERUNAARU FURANSOWA MATSUKU, ERITSUKU ORIBIE RONGU, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Pred. No. 1.26e-01;
0; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MATSUKU, B.F., RONGU, E.O. and Ueiku, K.T. .
DNA ARRANGEMENT FOR CODING DR BETA-CHAIN PART OF
ANTIGEN COMPOSITE, POLYPERPIIDE RELATED THERETO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10937..11116
/bound_moiety="RNA initiation site"
2404 c 3188 g 3227 t
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BIOGEN NV
OS human
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Best Local Similarity 89.1%;
Matches 41; Conservative
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Homo sapiens
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variable segment.

Homo sapiens (clone: K1A) (clone_lib: CGM1:YAC D4914) DNA; Homo sapiens (clone: K15) (clone_lib: CGM1:YAC D4914) DNA; Homo sapiens (clone: K26) (clone: L1b: CGM1:YAC D4914) DNA; Homo sapiens (clone: X20) (clone.lib: CGM1:YAC D4914) DNA; Homo sapiens (clone: K26) (clone_lib: CGM1:YAC D4914) DNA; Homo sapiens (library: ATCC L521) (clone_lib: Kai Wang's) DNA; Homo sapiens (library: ATCC L521) (clone: H137) (clone_lib: Kai Wang's) DNA; Homo sapiens (library: ReLa) (clone: H137) (clone_lib: Eric Lai's) DNA; Homo sapiens (library: sperm) (clone: H187) (clone_lib: Eric Lai's) DNA; Homo sapiens (clone: G15) (clone_lib: Kai Wang's) DNA; Homo sapiens (library: ATCC L521) (clone: H187) (clone_lib: Kai Wang's) DNA; Homo sapiens (clone: H187) (clone_lib: Kai Wang's) DNA; Homo sapiens (clone: A27) (clone_lib: CGM1:YAC 234 A6F6) DNA; Homo sapiens (clone: A27) (clone_lib: CGM1:YAC 234 A6F6) DNA; Homo sapiens (clone: A212partial) (clone_lib: CGM1:YAC 234 A6F6) DNA;
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/product="Pax-1 protein"
/db_xref="Ppx-1"

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Murinae; Mus.
1 (Dases 1 to 2619)
Chalepakis,G., Fritsch,R., Fickenscher,H., Deutsch,U., Goulding,M. and Gruss,P.
The molecular basis of the undulated/Pax-1 mutation
Cell 66, 873-884 (1991)
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Pred. No. 2.80e-01;
0; Mismatches 3; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57/BL6"
/dev_stage="8.5 day embryo"
/tissue_lib="lambda gt10"
244.2555
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Best Local Similarity 92.7%;
Matches 38; Conservative
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ORIGIN
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MEDLINE
FEATURES
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                                                                 REFERENCE
                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                              TITLE
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Homo sapiens (clone: A14) (clone_lib: CGM1: YAC 234 A6F6) DNA; Homo sapiens (library: sperm) (clone:H7.1) (clone_lib: Eric La1's) DNA; Homo sapiens (clone: H12.18) (clone_lib: Eric La1's) DNA; Homo sapiens (clone: A16) (clone_lib: Eric La1's) DNA; Homo sapiens (clone: A16) (clone: H130) (clone_lib: Eric La1's) DNA; Homo sapiens (clone: A16) (clone_lib: CGM1: YAC 234 A6F6) DNA; Homo sapiens (clone: C215) (clone_lib: CGM1: YAC 234 A72B3) DNA; Homo sapiens (clone: C21) (clone_lib: CGM1: YAC 234 A72B3) DNA; Homo sapiens (clone: C21) (clone_lib: CGM1: YAC 234 A72B3) DNA; Homo sapiens (library: ATCC 1521) (clone: X1) (clone: X6A) (clone_lib: Kai Wang's) DNA; Homo sapiens (library: ATCC 1521) (clone: X6A) (clone_lib: Kai Wang's) DNA; Homo sapiens (library: ATCC 151) (clone: X6A) (clone_lib: Kai Wang's) DNA; Homo sapiens (library: ATCC 1521) (clone: CBC1) (clone: CB
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Direct Submission
Submitted (25-JUN-1997)
This sequence overlaps section 2 of the human T cell receptor beta locus, Genbank Accession Number U66060, by 20616 bases.
Location/Qualifiers
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Rowen, L., Wang, K., Boysen, C., Ahearn, M.E., Charmley, P., Paeper, B., Lee, I., Chen, L., Trask, B., Nickerson, D., Seto, D. and Hood, L.
Sequence variation among several haplotypes in the human T cell receptor beta locus
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Rowen, L., Seto, J., Smit, A., Acharya, C., Ahearn, M.E., Ankener, M.,
Baskin, D., Bumgarner, R., Chen, L., Chen, N., Deshpande, P., Faust, J.,
Howard, S., Jerome, N., Koop, B.F., Lee, H., Loretz, C., Paeper, B.,
Zackrone, K. and Hood, L.
Sequence determination of the human T cell receptor beta locus:
Strategy and error analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rowen, L., Koop, B.F. and Hood, L.
The complete 685-kilobase DNA sequence of the human beta T cell
receptor locus
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Submitted (15-OCT-1994) L.Rowen leerowen@u.washington.edu
5 (bases 1 to 232650)
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/cell_line="CGM1, haplotype A"
/clone="A16"
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/organism="Homo sapiens"
/cell_line="CGM1, haplotype A"
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957..108
/note-"LINE; putative"
/rpt_family-"LIMA4A"
1294..1328
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                 misc_feature
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                                                                                                                                                                                                                                                   Submitted (25-JUN-1997) to the EMBL/GenBank/DDBJ databases. L.Rowen leerowen@u washington.edu
Lingr/Lingn, 166061; Release 97.06.
This sequence overlaps section 2 of the human T cell receptor beta locus, Genbank Accession Number U66060, by 20616 bases.
                                           Rowen L., Wang K., Boysen C., Ahearn M.E., Charmley P., Paeper B., Lee I., Chen L., Trask B., Nickerson D., Seto D., Hood L.; "Sequence variation among several haplotypes in the human T cell receptor beta locus";
                                                                                                                                                                       Submitted (15-OCT-1994) to the EMBL/GenBank/DDBJ databases.
L.Rowen leerowen@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="putative"
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4775 5155
Strategy and error analysis";
Unpublished.
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Gaps

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Direct Submission

Wu,C.H., Wang,N.M.Y. and Lee,M.F.

Direct Submission

L Submitted (04-SEP-1996) Medical Research, Taichung Veterans General Hospital, 160 Chung-Kang Road, Section 3, Taichung, Taiwan 40705, Republic of China

Republic of China

Republic of China

Republic of China

Submitted (11-JUL-1997) Medical Research, Taichung Veterans General Hospital, 160 Chung-Kang Road, Section 3, Taichung Veterans General Hospital, 160 Chung-Rang Road, Section 3, Taichung, Taiwan 40705, Republic of China

Sequence update by submitter

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="Cr-PII allergen"
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PDFKALYDAIRSPEFQSIISTLNAMPEYQELLQNLRDKGVDVDHFIELIRSWFGLP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 1024)
Wu,C.H., Wang,N.M.Y. and Lee,M.F.
Cloning of cDNAs encoding the American cockroach Cr-PII allergens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAUG9261 1024 bp mRNA INV 15-JUL-1997
Periplaneta americana Cr-PII allergen mRNA, partial cds.
UG9261
92253609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tracheata; Hexapoda; Insecta; Pterygota; Orthopteroidea; Dictyoptera; Blattidae; Periplaneta.

1 (bases I to 1024)
Mu,C.H., Hsieh,M.J., Huang,J.H. and Luo,S.F.
Identification of low molecular weight allergens of American cockroach and production of monoclonal antibodies
Ann Allergy Asthma Immunol 76 (2), 195-203 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Periplaneta americana
Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
                                                                                                                                                                                                                                                                                                                                            Score 35; DB 102; Length 232650;
Pred. No. 2.80e-01;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
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/note="LINE; putative"
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                                                                                                                                                                                                                                                                                                     annotations omitted.
                                                                                                                                                                                 /note="putative"
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                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      American cockroach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - awaiting approval of new feature
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                                                                                                                                                                                                                                                                                                                                            /note="translocation breakpoint; t(7:9); putative"
6654..6746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="RSS - awaiting approval of new feature key
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                                                                                                 complement(2280..2579)
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/gene="TCRBV2S1"
/note="RSS_heptamer -
key; putative"
                      1989..1997
/gene="TCRBV17S1A1T"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="Alu" <9153..9183 /gene="TCRBV2S1" /note="putative"
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2664..2756
                                                                                                                                                                                   /rpt_type=tandem
4775_5156
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9826..9864
/gene="TCRBV2S1"
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9833..9855
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in Unknown.

Unclassified.

Unclassified.

I (bases 1 to 1747)

S Boulton, T.G., Cobb, M.H., Yancopoulos, G.D., Nye, S. and Panayotatos, W.

Family of map2 protein kinases

L. Patent: US 5595904-A 1 21-7AN-1997;

Location/Qualifiers

I. 1777

Arganism="unknown"

NT 423 a 524 c 425 g 375 t
         .
Unknown.
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                        source
                                                                                                     TITLE
JOURNAL
FEATURES
                                                            REFERENCE
AUTHORS
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Query Match
3.4%; Score 34; DB 72; Length 1747;
Best Local Similarity 68.9%; Pred. No. 6.20e-01;
Matches 62; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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Search completed: Thu Feb 26 10:44:39 1998 Job time: 1537 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by Intelligenetics, Inc.

Thu Feb 26 10:45:00 1998; MasPar time 139.57 Seconds 817.716 Million cell updates/sec n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn Run on:

Tabular output not generated.

>US-08-874-460-1 (1-989) from US08874460.seq 989 Title: Description: Perfect Score:

N.A. Sequence:

TABLE default Gap Scoring table:

159651 seqs, 57698962 bases x 2 Searched:

Dbase 0; Query 0

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STD

Nmatch

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

n-geneseq30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part13 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33

Mean 9.188; Variance 6.978; scale 1.317 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		*					
Result							
No.	Score		Match Length DB	8	ព	Description	Pred. No.
υ	9/ 1	7.7	T047	7	910572	Human Natriuretic Pep	3.89e-24
•	2 70	7.1	1047	~	010572	Human Natriuretic Pep	4.25e-21
	3 47	4.8	204	-	N81164	Base substituted E.co	7.76e-10
•	4 45	4.6	91	σ	051746	Oligonucleotide probe	6.73e-09
-, ن	5 44	4.4	91	σ	051746	Oligonucleotide probe	1.97e-08
ů	5 41	4.1	204	Н	N81164	Base substituted E.co	4.74e-07
•	39	3.9	114	12	070465	Generic DNA sequence	3.84e-06
_	3 36	3.6	114	17	970468	Generic DNA sequence	8.38e-05
٠.	35	3.5	114	12	070466	Generic DNA sequence	2.31e-04
ĭ	35	3.5	130	31	T76152	Human vascular cell a	2:31e-04
H	35	3.5	190	31	T76452	Chymase antisense ol1	2.31e-04
H	35	3.5	1215	ო	N40067	Sequence of HLA-DR-be	2.31e-04
H	3 34	3.4	114	12	970467	Generic DNA sequence	6.29e-04
Ä	34	3.4	114	12	070469	Generic DNA sequence	6.29e-04
ä	5 34	3.4	114	12	070470	Generic DNA sequence	6.29e-04

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ALIGNMENTS

010572;
09-APR-1991 (first entry)
Human Natriuretic Peptide Receptor B.
NYRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase;
Hyperaldosteronism; glaucoma; guanyl cyclase. Domain 23..455
/label- extracellular domain
/note- "binds natriluretic peptides A,B and C]"
Domain 456..456
/label- transmembrane domain
pomain 479..1047 /label-cytoplasmic domain /note- "GC and protien kinase activity" Modified -site 24..26 Location/Qualifiers JT 1 Q10572 standard; DNA; 1047 BP. /label N-glycos_site Modified -site 277..279 /label N-glycos_site Modified -site 349..351 /label N-glycos_site Modified -site 600..602 /label N-glycos_site W09100292-A. /label signal sequence Protein 12 /label mature NPBR Domain /label N-glycos_site Modified -site 35..37 /label N-glycos_site Modified -site 161..163 /label= N-glycos_site Modified -site 244..246 Modified -site 195..197 /label- N-glycos_site RESULT DON SELLITER SELLITER

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RESULT ID N8 AC NE DT OE DE BE

186 196

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16

Matches

9/ 126

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Introducing random point mutations into nucleic acods -
Introducing random point mutations into nucleic acods -

by prepn of single stranded template, annealing a primer, elongation,
mislncorporation, completion of molecules and screening.

Disclosure; p; English.

Random point mutations were introduced into the alpha fragment of
E.coli beta-galactosidase. The wild type sequence was obtained as a
E.coli beta-galactosidase. The wild type sequence was bybridised to
it to generate a popn of DNA molecules which terminate at all
possible nucleotide positions within a specified region. The
variable 3' ends generated in this way are used as primers for
reverse transcriptase. Nucleotides are misincorporated by the
transcriptase and the molecules are completed to forms that can be
amplified and then expressed in a suitable host-vector system.
The sequence covers all 176 difft base substitutions, most of which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 dchvgccgymrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyv 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           491 GCAAGAGGAATGICTCCCTCCTGAIATCAGCTAATTCAGGACTGTGAGCCGGCTCATTTC 550
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Pred. No. 7.76e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 G;
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Pred. No.
                                       Location/Qualifiers
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24-WAY-1993; 108325.
26-WAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
Shank DD, Spears PA;
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primer_bind 187..204
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Best Local Similarity 12.4%;
Matches 14; Conservative
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Q51746 standard; cDNA; 91
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      Escherichia coli.
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                                                                                                                        snynannsavdnknyhdndnnngngcvynaasvarnashwrnnnntagavasgnsakndh 135
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                                                                 gvrnngarnntnavvnnnhnnsyawawnrvgnavanavnangrannvdnrnvssnnngac 75
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249; Mismatches 593;
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0; Gaps

108 Others;

11 T;

Length 204; 40; Indels

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for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        claim 3; Page 14; 23pp; English.
Oligonuclectide probe MK14-A consists of nucleotides 5-95 of (051735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Seequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                 nseq
Q51746;
31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 93-378844/48.
New oligo:nucleotide probes specific for Mycobacteria – used
detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 91;
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6.73e-09;
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Tidentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins PT screening a recombinant vector library expressing fusion proteins PT screening a recombinant vector library expressing fusion proteins PT screening a recombinate by a binding domain and an effector domain bisclosure: Page 35: 255pp: English.

CC 370468 is a generic DNA Sequence used to generate random TSAR (Totally CC Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)11(TGC)(NNB)52(NNB)7(TGC)(NNB)10Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68.

CC other specifies generated by these generic sequences are shown in R65151-54. TSARs are concatenated by these generic sequences are shown in CR65151-54. TSARs are concatenated by these generic sequences are shown in CR65151-54. TSARs are concatenated by these generic sequences are shown in CR65151-54. TSARs are concatenated by these generic sequences are shown in CC chemically or biologically active They may further comprise a linker comprising at least two functional regions - a binding domain with the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compress comprising a TSAR binding domain can be used in vivo to CC deliver a chemically to x biologically active molety, eq metal lon, call the force cell. They can also replace the function of macromolecules, eq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
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                                                                                                                      6 banbanbanbanbtgcanbanbanbanbanbanbanbanbanbanbannananana 65
                                                                                                                                                                                                                                                                                                                                                       Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affility reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                           Gaps
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                                                                                                                                                                66 bnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbtgcnnbnnb 114
                                                                                                                                                                                                       222 CGCCTGGACTTACCGGATCCAGGAGGTGAGCGGGAGCTGCAATCTGCCT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 114;
  Length 114;
Score 39; DB 12; Length 114
Pred. No. 3.84e-06;
33; Mismatches 70; Indels
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Pred. No. 8.38e-05;
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/note= "this sequence represents '2'; Z can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence of 6, 9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Q70468 standard; DNA; 114 BP.
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FOURSE DM, KAV DV.
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3.98;
5.58;
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                                           6; Conservative
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US-176500.
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  Query Match
Best Local Similarity
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                                                                                                                                                                                                     05-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR-9 petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker;
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                                   207 GGCTGTGCTCCGGCGCGCGTTTACCGGATCCAGGAGGTGAGCGGGAGC 258
63 bnabaabaabaabaabtgcaabaabaabaabaabaabaabaabaabaabaab 114
                                                                                                                                                                                                                                                                                                                 rapid; detection; screening; treatment; generic; ss.
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/note= "this sequence represents
                                                                                                                                                       standard; DNA; 114 BP
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(UYNC-) UNIV NORTH CAROLINA.
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US-176500.
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94-279739/34.
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Best Local Similarity
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147 TGTCCACACCCAAGGTGTCTTTGAGGACTGCTGCCTGGCCTACCACTACCCCATTGGGTG 206

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Gaps

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74; Indels

33; Mismatches

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Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins or comprising a binding domain and an effector domain bisclosure; Page 35; 255pp; English.

Disclosure; Page 35; 255pp; English.

O70467 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)16(TGC)(NNB)12(NNB)16(TGC)(NNB)1X. X and Y are flanking restriction sites (X is not the same as Y) that are controlled further. Other generic sequences are shown in Q70466-68.

Other specific peptides generated by these generic sequences are shown in CR65151-34. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chanically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues positioned in, or flanking, the unpredicted or variant residues seed in vivo to deliver a chemically or biologically active molety, eg. metal lon, calling and the function of macromoleuse, eg. cell. They can also replace the function of macromoleuse, eg.
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07-ARR-1995 (first entry)
Generic DNA sequence to generate a random TSAR peptide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concatemented heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 12; Length 114;
Pred. No. 6.29e-04;
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sequence of 6,9 or 12 nucleotides (see
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Q70469 standard; DNA; 114 BP.
                                                                                                                                  30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWIKES DM, KAY BK;
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3.6%;
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P-PSDB; R65153.
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US-013416. US-176500. US-189331.

31-JAN-1994;

T00077

01-FEB-1994;

18-AUG-1994.

01-FEB-1993; 30-DEC-1993;

comments)" WO9418318-A.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Generic DNA sequence to generate a random TSAR peptide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                         3.4%; Score 34; DB 12; Length 114; 5.5%; Pred. No. 6.29e-04; tive 31; Mismatches 73; Indels
                     Identifying proteins or peptide(s) which bind a ligand screening a recombinant vector library expressing fusic
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C;
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(UYNC-) UNIV NORTH CAROLINA.
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Generic DNA sequence to ger
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01-FEB-1994; U00977.
01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
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Kay BK;
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Best Local Similarity
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P-PSDB; R58378.
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.	000
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:1on: (1 Score: 98 Juence: 98	0000000
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Searched: 333433 segs, 126143548 bases x 2	000
Post-processing: Minimum Match 0% Listing first 45 summaries	000
Database: STS 1:STS1 2:STS2 3:STS3 4:STS4 5:STS5 6:STS6 7:STS7 8:STS8 9:STS9 10:STS10 11:STS11 12:STS12 13:STS13 14:GDEST1 15:GDEST2 16:GDEST3 17:GDEST5 19:GDEST5 20:GDEST7 21:GDEST8 22:GDEST5 29:GDEST5 19:GDEST13 25:GDEST12 26:GDEST13 27:GDEST19 23:GDEST15 29:GDEST13 30:GDEST12 26:GDEST13 27:GDEST19 33:GDEST25 39:GDEST213 35:GDEST22 36:GDEST13 27:GDEST24 38:GDEST25 39:GDEST25 40:GDEST27 41:GDEST23 37:GDEST24 38:GDEST25 39:GDEST26 40:GDEST27 41:GDEST23 37:GDEST24 38:GDEST25 39:GDEST25 50:GDEST5 51:GDEST 67:GDEST24 38:GDEST25 69:GDEST3 60:GDEST3 60:GDEST3 73:GDEST25 60:GDEST3 77:GDEST25 60:GDEST27	RES OOD SOURCE RES OOD SOURCE OOO
Statistics: Mean 11.575; Variance 5.079; scale 2.279	4 H
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	r COM

SUMMARIES

% Query Score Match Length DB ID

Result Query No. Score Match Leng

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g2264178
                                                                                                             human.
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Email: Robert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                              National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                 AA501896 319 bp mRNA EST 10-JUL-1997
ng19q09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone 929920.
AA501896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: paMP10; mRNA made from liposarcoma, c
made by oligo-dT priming. Non- directionally cloned.
Size-selected on agarose gel, average insert size 6
Reference: Krizman et al. (1996) Cancer Research
56:5380-5383."
/clone="929920"
/tissue_type="liposarcoma"
/lab_host="DH10B"
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                                                                                                        Length 319;
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                                                                                                     Score 36; DB 69; Length 319
Pred. No. 1.59e-07;
0; Mismatches 12; Indels
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Pred. No. 1.59e-07;
0; Mismatches 12; Indels
                               /tissue_type="liposarcoma"
/lab_host="DH10B"
arNA
-(1..>319
Sequence 319 BP; 109 A; 52 C; 45 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert Length: 945 Std Error: 0.00 Seg primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 253.
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/clone="929920"
/clone_lib="NCI_CGAP_Lip2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
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                                                                                                    3.6%;
Best Local Similarity 80.0%;
Matches 48; Conservative
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Similarity 80.0%;
48; Conservative
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Unpublished (1997)
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Best Local Similarity
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Tel: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,
Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
AA523466 221 bp mRNA EST 17-JUL-1997 ni63h06.s1 NCI_CGAP_F112 Homo sapiens cDNA clone 981563 similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pAMP10; mRNA made from metastatic prostate lesion of the bone, cDNA made by oligo-dT priming.
Non-directionally cloned. m2se-selected on aganose age, average insert size 600 bp. Library made by D. Krizman,
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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B-JUL-1997 (Rel. 52, Last updated, Version 1)
n163106 s1 NCL_GGAP_Pr12 Hono sapiens cDNA clone 981563 similar
gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
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Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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/lab_host="DH10B"
<1..>221
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Pred. No. 7.69e-07;
0; Mismatches 4; Indels
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High quality sequence stop: 171.
Location/Qualifiers
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/sex="male"
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/organism="Homo sapiens"
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Best Local Similarity 90.7%;
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                         T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. RNA provide
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
www-bio.llnl.gov/bbrp/image/image.html
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Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                            AA490904 443 bp mRNA EST 25-JUN-1997
aa52b07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 824533 3'.
AA490904
22220077
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                                                                                                 normalized by Bento Soaresand M.Fatima Bonaldo."/clone="876090"
/clone_lib="Soares mouse mammary gland NDMMG"
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                                                                                                                                                                                                               Score 35; DB 84; Length 247; Pred. No. 7.69e-07;
                                                                                                                                                                                                                                       0; Mismatches 14; Indels
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High quality sequence stop: 337.
Location/Qualifiers
                                                                                                                                                   /dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                      /sex-"male"
                                                                                                                                                                                                              3.5%;
Similarity 77.8%;
49; Conservative
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3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo." /clone="834533" /clone="834533"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
//organism="Took of partial p
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Robert_Strausberg@nih.gov Tissue Procurement: Louis M. Staudt,
M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D. cDNA Library
Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA
Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by:
Washington University Genome Sequencing Center Clone distribution:
NCI-CGAP clone distribution information can be found through the
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www-bio.llnl.gov/bbrp/image/image.html Seq primer: -41ml3 fwd. ET
from Amersham High quality sequence stop: 337.

Location/Qualifiers
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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03-JUL-1997 (Rel. 52, Last updated, Version 1)
aa52b07.sl NCI_CGAP_GCB1 Homo sapiens cDNA clone 824533 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 443;
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/lab_host="DH10B"
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/clone="824533"
/clone_lib="NCI_CGAP_GCB1"
                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="germinal center B
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94 c 79 g
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Best Local Similarity 80.7%;
Matches 46; Conservative
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Unpublished.
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1-632

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Tel: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., M. Fatima
Dh.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E., Consortium/Link at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project
Washington University School of MedicineP 4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-FEB-1997 (Rel. 50, Created)
15-FEB-1997 (Rel. 50, Last updated, Version 1)
mw16e06.rl Soares mouse 3NME12 5 Mus musculus cDNA clone 670882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae;
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High quality sequence stop: 74.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                 www-bio.llnī.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                   Contact: Robert Strausberg, Ph.D.
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MMI140745 standard; RNA; EST; 197
AA221995;
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Matches 39; Conservative
      Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                 1..632
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BASE COUNT
ORIGIN
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    JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism-"Homo sapiens"
//organism-"Homo sapiens"
//organism-"Homo sapiens"
//organism-"Homo is Site_1: Bco RI: lst strand cDNA
polylinker; Site_1: Not I; Site_2: Bco RI: lst strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louls M.Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dI) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
/clone="825440"
/clone="1b="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA504326 632 bp mRNA EST 02-JUL-1997 aa61e05.s1 NCI_CGAP_GCB1 HOMO Sapiens CDNA clone 825440 3' similar AA504326
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:
Robert_Strausberg@nih.gov Tissue Procurement: Louis M. Staudt,
M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D. CDNA Library
Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. CDNA
Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by:
Washington University Genome Sequencing Center Clone distribution:
NCI-CGAP clone distribution information can be found through the
aa61e05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 825440 3' similar
to gb:x64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Seq primer: -40ml3 fwd. ET
from Amersham High quality sequence stop: 74.

Key
Location/Qualifiers
                                                                                                                                                                                                   NCI-CGAP;
"National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                              Homo sapiens (human)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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87 A; 166 C; 172 G; 207 T; 0 other;
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Pred. No. 7.69e-07;
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Local Similarity 90.7%;
hes 39; Conservative
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                                                                                                                                                                                                                                             Tumor Gene Index";
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                                                                                                                                                                                                                                                                       Unpublished.
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RESULT 14 LOCUS

MRNA

SHIHHH

Matches

8

ORGANISM

ACCESSION

KEYWORDS

AUTHORS TITLE

REFERENCE

source

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Gaps

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US-08-874-460-2.rag

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在各种的人,我们也是我们的人,我们也是我们的人,我们也不是我们的,我们也不是我们的,我们也不会有什么的,我们也不会有什么的,我们的人,我们的人,我们的人,我们的人		***************************************
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*		*

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Feb 26 10:16:16 1998; MasPar time 6.46 Seconds 320.550 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-874-460-2 (1-149) from US08674460.pep 1099 Description:

Perfect Score:

1 MNLWLLACINAGFLGAWAPA........NPISSSKRNVSLLISANSGL 149 Scoring table:

Sequence:

PAM 150 Gap 11

111726 segs, 13889129 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq30
lipart1 2.part2 3.part3 4.part4 5.part5 6.part6 7.part7
8.part8 9.part9 10.part10 11.part11 12.part12 13.part13
14.part14 15.part15 16.part16 17.part17 18.part18
19.part19 20.part20 21.part21 22.part22 23.part23

Mean 31.118; Variance 123.942; scale 0.251 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	2.19e-05	6.20e-05	1.35e-03	1.65e-03	1.23e-02	1.50e-02	1.50e-02	1.50e-02	1.50e-02	1.50e-02	1.50e-02	1.50e-02	1.50e-02	4.91e-02	4.91e-02	5.98e-02	5.98e-02	7.27e-02	1.58e-01	1.58e-01
	Description	Chemokine beta-9.	Pancreas expressed ch	Mouse thymus and acti	Stem cell mobilising	Human thymus and acti	Human chemokine beta-	Human chemokine beta-	Human chemokine beta-	Stem cell mobilising	Human chemokine beta-	Human cytokine beta-8	Macrophage inflammato	Human eosinophil-expr	Human eosinocyte CC t	Human eotaxin.	Human chemokine beta-	Liver expressed chemo	Pancreas expressed ch	LD78 Glu55>Arg, Glu56	Stem cell mobilising
	£	R81567	W00668	W14918	W17664	W14917	W16318	W16317	W16316	W17663	W16315	W07202	R76126	W05186	W14990	W10099	R93086	R95690	W00667	R38942	W17661
	80	17	20	23	23	23	23	23	23	23	23	73	13	22	23	22	17	18	20	7	23
	Watch Length DB	134	134	93	79	94	75	16				120	121	137	97	97	96	96	97	69	70
a p (Match	14.3	13.8	12.5	12.4	11.5	11.4	11.4	11.4	11.4	11.4	11.4	11.4	11.4	10.8	10.8	10.7	10.7	10.6	10.3	10.3
	Score	157	152	137	136	126	125	125	125	125	125	125	125	125	119	119	118	118	117	113	113
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Human monocyte chemot Human monocyte chemot LD78 Trp57>Ala. Guinea pig eosinocyte	LD/8 1701-Ala. LD/8 Gln33-Ser. Stem cell mobilising LD/8 Tyr61-Asp. LD/8 Trp57-Leu.		LD78 Ser46>Glu. LD78 Glu55>Gln, Glu56 LD78 Asp64>Arg. LD78 Phe28>Glu, Gln48 LD78 Asp64>Ser.	
R85779 W07845 R39123 W14991	R39089 W17660 R39127 R39125	R39106 R38980 R38973 R39105	R38963 R39137 R39132 R38940 R38983	R38981 R39109 W01805 R39108 R38960 R70252
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ALIGNMENTS

Olocy-1996 (first entry)
Chemokine beta-9.
Human, chemokine beta-9; Ck beta-9; breast lymph node; chemokine;
eotaxin; inhibition; bone marrow stem cell colony formation;
cancer chemotherapy; leukaemia; epidermal keratinocyte proliferation;
psoriasis; solid tumour; autoimmune disease; IL-2 biosynthesis. Location/Qualifiers T 1 R81567 standard; Protein; 134 AA. 06-JUN-1995; U06260. 23-AUG-1994; US-294251. (HUMA-) HUMAN GENOME SCI INC. Adams MD, Li H; Peptide 1..23
/note= "Leader sequence"
Protein 24..134
/note= "Mature CK beta-9"
W09606169-Al. WPI; 96-151372/15. N-PSDB; T18015. Homo sapiens. RESULT

for leukaemia. They can also be used to inhibit epidermal keratinocyte proliferation for treatment of psoriasis. They may be used to treat solid tumours by stimulating the invasion and activation of host defence cells, e.g. cytocxic r cells and macrophages. They act to enhance host defences against resistant chronic infections, and to treat autoimmune disease and lymphocytic leukaemia by inhibiting T cell proliferation by the inhibition of IL-2 biosynthesis. beta-9 mutation(s)

Claim 12; Page 41; 55pp; English.

This sequence represents human chemokine beta-9 (Ck beta-9). The polynucleotide encoding Ck beta-9 was discovered in a cDNA library derived from a human breast lymph node. Ck beta-9 is structurally related to the chemokine family. It exhibits the highest degree of homology to eotaxin with 32* identity and 69* similarity over a stretch of 75 amino acids. The four spatially conserved cysteine residues found in chemokines are also found in Ck beta-9. Ck beta-9 polypeptides may be used to inhibit bone marrow stem cell colony formation as adjunct protective treatment during cancer chemotherapy and for leukaemia. They can also be used to inhibit epidermal keratinocyte Human chemokine beta-9 polynucleotide(s), polypeptide(s) and antagonists - useful in treatment of e.g. leukaemia, tumours, chronic infections and auto-immune disorders and diagnosis of Ck

English.

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29 etnsecskpgvif-ltkkgrrfcanpsdkgvgvcmrmlkldtrik 72
Claim 4; Page 18; 26pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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97-212900/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and antiinflammatory agost transfer of claim 10; pages 58-59; 102pp; Japanese.
The present sequence is human thymus and activation regulated chemokine (TARC), which is similar to CC type chemokines and expressed in peripheral blood monocytes under immunological stimulus, e.g. phyto-haemagglutinin or soluble cytokine, and the thymus, but not by the spleen. TARC is active against CCR4 expressing cells, e.g. T cells, peripheral lymphocytes and activated peripheral T cells, especially Hut 78, Hut 102, Jurkat, MT2 and MT4 cells, and is useful as an immunomodulator or anti-inflammatory agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New CC-chemokine-like protein - is expressed by peripheral blood monocytes under immunological stimulus, useful as immunomodulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC type;
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Pred. No. 1.23e-02;
23; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-1997 (first entry)

Human thymus and activation regulated cytokine (TARC).
Human; thymus; activation; regulation; chemokine; TARC;
peripheral; blood; monocyte; CCR4; T cell; lymphocyte;
immunomodulatation; inflammation.
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Chemokine beta-8; Ck beta-8; bone marrow; stem cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 -rdalvfvtvqgraicsdpnnkrvknavkylgs 90
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27-SEP-1996; J02801.
13-MAR-1995; JP-056044.
27-SEP-1995; JP-249457.
(SHIO) SHIONOGI & CO LTD.
Imai T, Yoshida T, Yoshie O;
WPI; 97-212853/19.
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27-SEP-1996; U15592.
29-SEP-1995; US-004517.
(SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                        standard; Protein; 94 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 33.3%;
Matches 31; Conservative
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WPI; 97-212900/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 AA;
                                           64 lmqhld 69
                                                                                                                             86 AMKLLD 91
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WO9711969-A1.
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WO9712041-A1.
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W14917
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11D 24

12D 24

13D 24

13D 24

13D 25

13D 25
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Novel polypeptides (Wi6315-18) are truncated forms of human chemokine beta-8 (Ck beta-8), respectively comprising the 82, 77, 76 and 75 C-terminal amino acids of full-length Ck beta-8. They can expressed in E. coli, CoS and 859 cells using vectors designed to express Ck beta-8 CDNA. They can be administered to patients requiring Ck beta-8 (Claimed), e.g. to protect bone marrow stem cells from chemotherapeutic agents, remove leukaemic cells, treat postlasis and solid tumours or stimulate wound healing. When Ck psorlasis and solid tumours or stimulate wound healing. When Ck claimed) e.g. to treat aplastic anaemia, myelodysplastic syndrome, asthma and arthritis. The polypeptides can be used to identify cathma and arthritis. The polypeptides can be used to identify assays can detect diseases to produce antibodies. Diagnostic assays can detect diseases or susceptibility to diseases relating to under- and over-expression of Ck beta-1; under-expression the contractions may be detected at
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Novel polypeptides (W16315-18) are truncated forms of human chemokine beta-8 (Ck beta-8), respectively comprising the 82, 77, 6 and 75 C-terninal amino acids of full-length Ck beta-8. They were expressed in E. coli, CoS and 5f9 cells using vectors designed to express Ck beta-8 cDNA. They can be administered to patients credibling Ck beta-8 cDNA. They can be administered to patients credibling Ck beta-8 (claimed), e.g. to protect bone marrow stem cells from chemotherapeutic agents, remove leukaemic cells, treat psoriasis and solid tumours or stimulate wound healing. When Ck beta-8 inhibition is necessary, an antagonist can be administered (claimed) e.g. to treat aplastic anemnia, myelodysplastic syndrome, asthma and arthritis. The polypeptides can be used to identify antipagonists and as immunogens to produce antibodies. Diagnostic assays can detect diseases or susceptibility to diseases relating to under- and over-expression of Ck beta-1; under-expression claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Human chemokine beta 8 short form.

Chemokine beta-8; Ck beta-8; bone marrow; stem cell;

chemotherapy; therapy; leukaemia; cancer; tumour; psoriasis;

wound healing; vulnezary; aplastic anaemia; asthma; arthritis;

myelodysplastic syndrome; antagonist.
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Pred. No. 1.50e-02;
11; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 125, DB 23; Length 75
Pred. No. 1.50e-02;
11; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                etnsecskpgvif-ltkkgrrfcanpsdkgvqvcmrmlkldtrik 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 18; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .r 7
W16317 standard; Protein; 76 AA.
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(SMIK ) SMITHKLINE BEECHAM CORP.
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Best Local Similarity 42.2%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.4%;
Similarity 42.2%;
19; Conservative
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Rosen CA, Ruben

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Naryob Ayrose.

1-gamma - used in immuno-regulation includding inflammatory activity, haematopolesis, treatment of psoriasis or solid tumours. Claim 10; Figure 1; 60pp; English.

Human macrophage inflammatory protein-3 (MIP-3) is used in therapeutic and diagnostic applications for detecting and treating infections, cancer, inflammation, myelopoletic dysfunction and autoimmune diseases. Antagonists, Jihibbitors of MIP-3 are used to treat diseases involving overexpression of MIP-3, including silicosis, arteriosclerosis, autoimmune and chronic inflammatory and infective diseases, aplastic anaemia,
                    (HUMA-) HUMAN GENOME SCI INC.
Adams MD, Li H, Rosen CA, F
WPI; 95-240404/31.
08-MAR-1994; US-208339
                                                                                               N-PSDB; Q94092.
                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
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W05186 :
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Matches
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Screening
Claim 1: Page 57: 93pp; English.

Human chemokine beta-8 (Ckbeta8) is an attractant for leucocytes and is fluman chemokine beta-8 (Ckbeta8) is an attractant for leucocytes and is fluvolved in the regulation of immune responses and inflammation, e.g.

Stimulating synthesis of other cytokines. DNA encoding Ckbeta8

Confemcherapeutic agents, for eliminating bone marrow against chemotherapeutic agents, for eliminating leukaemia cells (by inducing apottosis), Stimulating an immune response and regulating haematopolesis (inhibiting proliferation and differentiation of cells) and lymphocyte confemces, to increase host defences against chronic and soute infection and to stimulate wound healing. Since Ckbeta8 also increase vascular permeability, it can be used to treat stroke, thromobocytosis, pulmonary embolism and myeloproliferative disease, and for identification of embolism and myeloproliferative disease, and for identification of production of it.1 and TNF-alpha and to treat e.g. aplastic anaemia, myelodysplastic syndrome, asthma, arthritis (and many other autoimmune and inflammatory diseases), infections, endoctoxic shock,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and inflammatory diseases), infections, endotoxic shock, atherosclerosis, allergy etc. Ckbeta8 and DNA encoding it may also be
                                                                                                              02-JUL-1997 (first entry)

Human cytokine beta-8: a chemoattractant for leukocytes.

Leukocyte; attractant; affinity; leukaemia; immunity; wound healing; diagnosis; drug screening; inflammation; haematopoiesis regulator; psoriasis; stroke; thrombocytosis; pulmonary embolism; asthma; arthritis; aplastic anaemia; endotoxic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding the new human chemokine beta-8 - with chemo:attractant activity for leucocytes, for treating leukaemia, stimulating immunity and wound healing, also for diagnosis and drug
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Pred. No. 1.50e-02;
11; Mismatches 12; Indels
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Macrophage inflammatory protein-3.
Macrophage inflammatory protein-3; therapeutic; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 etnsecskpgvif-ltkkgrrfcanpsdkgvgvcmrmlkldtrik 116
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                                                                                                                                                                                                                                                                                            Location/Qualifiers
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R76126 standard; Protein; 121 AA.
                                          T 11
W07202 standard; Protein; 120 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 11.4%;
Best Local Similarity 42.2%;
Matches 19; Conservative
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"signal peptide"
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05-MAY-1995; US-446881.
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22-DEC-1993; US-173209
                                                                                                                                                                                                                                                                                                                                       /label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                       mat_protein
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                                                                                                                                                                                                                                                                   Homo sapiens
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WO9517092-A.
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                                                                                          W07202;
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ID R7
AC R7
DT 02
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CS HC
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FT 
                                          RESULT
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New human ecosinophil-expressed chemokine - used for producing

New human ecosinophil-expressed chemokine - used for producing

Inhibitors for treatment of e.g. ecosinophilia, inflammation,

allergies, asthma, leukaemia and lymphoma

Claim 9; Page 35; 68pp; English.

This is the amino acid sequence of a novel human ecsinophil-expressed

Chemokine (EEC). The gene sequence was isolated from human ecsinophil

CDNA library constructed from CDNA generated from mRNA purified from

cosinophils from a male caucasian diagnosed with Hypereosinophilic

Syndrome. The CDNA clones obtained were sequenced and encoded proteins

were searched for homology with databases. This sequence was found to

be homologous but different from other C-C chemokine family members.

CC be homologous but different from other C-C chemokine family members.

CC EEC-specific antibodies, antiseense oligonuclectides and other inhibitors

are useful for the treatment of ecsinophila, inflammation or any disease

invalving an altered number of ecsinophila, e.g., viral, bacterial,

fungal or parasitic infection, mechanical injury associated with trauma;

fungal or parasitic infection, mechanical injury associated with trauma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-5403-1997 (first entry)
Human eosinophil-expressed chemokine protein sequence.
Human, eosinophil-expressed chemokine; Hypereosinophilic Syndrome; homology; antibody; antisense; inhibitor; eosinophilia; inflammation; viral; bacterial; fungal; parasitic; infection; mechanical injury; trauma; hereditary allergy; asthma; leukaemia; lymphoma.
                                                                                                                                                Gaps
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                                                                      11.4%; Score 125; DB 13; Length 121; 42.2%; Pred. No. 1.50e-02;
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                                                                                                    Pred. No. 1.50e-02;
11; Mismatches 12; Indels
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Pred. No. 1.50e-02;
11; Mismatches 12;
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42.28;
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13-APR-1995; US-421144.
                                                                                                       Local Similarity
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WPI; 96-477132/47.
121 AA;
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Search completed: Thu Feb 26 10:16:47 1998 Job time : 31 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Feb 26 10:17:06 1998; MasPar time 8.84 Seconds 513.408 Million cell updates/sec

Tabular output not generated.

Title: >US-08-874-460.2
Description: (1-149) from US08874460.pep
Perfect Score: 1099

Sequence: 1 MNLWLLACLVAGFMGAWAPA.....NPISSSKRNVSLLISANSGL 149

Scoring table: PAM 150 Gap 11

Searched: 95051 seqs, 30469580 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir53
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann11 15:unann12 17:unenc
18:unrev

Statistics: Mean 41.426; Variance 82.134; scale 0.504

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 122 11.1 97 6 JC4912 2 116 10.6 116 16 14955 gene C10 protein - m 3 112 10.2 96 6 148099 macrophage inflammat 4 105 9.6 9.2 6 JC2478 macrophage inflammat 5 106 9.3 92 6 JC2478 macrophage inflammat 6 102 9.3 92 6 A30574 T-cell activation pr 7 102 9.3 99 6 JC2417 monocyte chemoattrac 8 101 9.2 148 6 JC2417 monocyte chemoattrac 9 100 9.1 93 6 B35673 LD78-beta protein LT 10 98 8.9 92 6 A33393 macrophage inflammat 11 97 8.8 476 16 JC4646 bone morphogenetic pr 12 97 8.8 476 16 JC4646 bone morphogenetic pr 13 95 8.6 571 10 S52750 dehRI protein - Pseu 14 92 8.4 91 2 A28815 monocyte chemoattrac 15 91 8.3 341 10 S51865 trsf protein - Pseu 16 91 8.3 341 10 S51865 trsf protein - Pseu 17 91 8.3 534 9 S55635 DNA helicase-primase 18 91 8.3 114 3 ETABL 19 90 8.2 114 3 ETABL 20 114 3 ETABL 20 114 3 ETABL 21	Result . No.	Score	% Query Match	* Query Match Length DB	03	а	Description	Pred. No
116 10.6 116 16 149555 gene C10 protein 112 10.2 96 148099 cetaxin precursor 105 9.6 96 502552 macrophage inflamm 106 9.6 9.6 502478 macrophage inflamm 102 9.3 99 6 502417 monocyte chemoatt 101 9.1 93 6 502417 monocyte chemoatt 100 9.1 93 6 502417 monocyte chemoatt 100 9.1 93 6 502573 LD78-beta protein 98 8.9 92 6 5025750 LD78-beta protein 97 88 476 16 502750 dehRI protein P 92 8.6 571 10 552750 dehRI protein P 92 8.4 91 2 524578 monocyte chemoatt 91 8.3 341 10 5554578 monocyte chemoatt 91 8.3 341 10 555458 macrophage in Taspenda 18.3 341 10 555458 monocyte chemoatt 91 8.3 341 10 555458 Machianse-prim 18.3 847 10 535418 modocyte chemotac 91 8.3 847 10 535418 modocyte chemotac 88 8.0 288 15 845803 8-coll-restricted	1	122	11.1	97	ေ	JC4912	eotaxin - human	5.82e-05
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91 8.3 847 10 S35418 mdoH protein - 90 8.2 114 3 ETMSL lymphotactin pr 88 8.0 288 15 A45803 B-cell-restrict	17	91	89.3	534	σ	S55635	DNA helicase-primase	1.24e+00
90 8.2 114 3 ETMSL lymphotactin precu 88 8.0 288 15 A45803 B-cell-restricted	18	91	8.3	847	10	S35418	mdoH protein - Esche	1.24e+00
88 8.0 288 15 A45803 B-cell-restricted	19	90	8.2	114	ო	ETMSL	lymphotactin precurs	1.66e+00
	20	88	8.0	288	12	A45803	B-cell-restricted an	2.95e+00

2.95e+00 3.93e+00 3.93e+00 3.93e+00 5.21e+00 5.21e+00 5.21e+00 6.90e+00 6.90e+00 1.20e+01 1.20e+01	1.20e+01 1.58e+01 1.58e+01 1.58e+01 1.58e+01 1.58e+01
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ALIGNMENTS

JC4912 *type complete ectaxin - human #formal_name Homo sapiens *common_name man 01-Nov-1996 *sequence_revision 01-Nov-1996 *text_change	JC4912 JC4912 JC4912 JC4912 Bartels, J.; Schlueter, C.; Richter, E.; Noso, N.; Kulke, R.; Christophers, E.; Schroeder, J.M. Biochem. Blophys. Res. Commun. (1996) 225:1045-1051 Human dermal fibroblasts express eotaxin: Molecular cloning, mRNA expression, and identification of eotaxin sequence	variants. cession JC4912 ##status preliminary ##molecule_type mRNA	#domain signal sequence #status predicted #label SIG\ #product eotaxin #status predicted #label MAT #length 97 #molecular-weight 10790 #checksum 448 11.1%; Score 122; DB 6; Length 97;
RESULT 1 ENTRY TITLE ORGANISM DATE	ACCESSIONS REFERENCE #authors #journal	#accession ##status ##status ##molecule, ##residues ##cross.re, ##cross.re ##experimen COMMENT This i KEYWORDS FFATION	1-18 19-97 SUMMARY Query Match

Query Match 11.1%; Score 122; DB 6; Length 97; Best Local Similarity 32.6%; Pred. No. 5.82e-05; Matches 30; Conservative 21; Mismatches 34; Indels 7; Gaps

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Db 62 vif-ktklakdicadpkkrwyddsmkylddks 92 || | | :||:|||||:: Qy 63 AIFYLPKRHRKVCGNPKSREVQRAMKLLDARN 94

RESULT 2 149555 #type complete gene C10 protein - mouse

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#authors Zipfel, P.F.; Balke, J.; Irving, S.G.; Kelly, K.; Siebenlist, U.

#journal J. Immunol. (1989) 142:1582-1590

#title Mitcopenic activation of human T cells induces two closely related genes which share structural similarities with a new family of secreted factors.

#cross-references MUID:89140347
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Mol. Cell. Biol. (1990) 10:3646-3658
Structures of human genes coding for cytokine LD78 and their
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Jose, P.J.; Adcock, I.M.; Griffiths-Johnson, D.A.; Berkman, N.; Wells, T.N.C.; Williams, T.J.; Power, C.A. Biochem. Biophys. Res. Commun. (1994) 205:788-798 fortaxin: Cloning of an eoslnophil chemoattractant cytokine and increased mRNA expression in allergen-challenged
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DNA Cell Biol. (1990) 9:589-602
Three human homologs of a murine gene encoding an inhibitor
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#product eotaxin #status predicted #label MAT\
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T This protein is identified as a potent eosinophil c
FICATION #superfamily macrophage inflammatory protein
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#authors Obaru, K.; Fukuda, M.; Maeda, S.; Shimada, K.
#journal J. Biochem. (1986) 99:885-894
#title A CDNA clone used to study mRNA inducible in human tonsillar
#cross-references WUID:86223879
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#formal_name Sus scrofa domestica #common_name domestic pig
24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change
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Biochen. Biophys. Res. Commun. (1994) 205:148-153
Porcine luteal cells express monocyte chemoattractant protein-2 (MCP-2): Analysis by cDNA cloning and northern
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##residues 1-92 ##label BLU
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#title Resolution of the two components of macrophage inflammatory protein 1, and cloning and characterization of one of those components, macrophage inflammatory protein 1 beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors Brown, R.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.
#journal J. Immunol. (1989) 142:679-687
#title A family of small inducible proteins secreted by leukocytes are members of a new superfamily that includes leukocyte and fibroblast-derived inflammatory agents, growth factors, and indicators of various activation processes.
#cross.references MUID:89093958
#accession A30552
                                                                                                              J. Exp. Med. (1988) 167:1939-1944 Cloning and characterization of a CDNA for murine macrophage inflammatory protein (MIP), a novel monokine with inflammatory and chemokinetic properties.
                                                                                                                                                                                                                                             ##nolecule_type mRNA
##residues 1-48,'E',50-90,'I',92 ##label DA2
##cross-references EMBL:X12531
##note the authors translated the codon GAG for residue 49 as
Asp and ATT for residue 91 as Asn
##note the sequence has been corrected in reference A53885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sherry, B.; Tekamp-Olson, P.; Gallegos, C.; Bauer, D.;
Davatelis, G.; Wolpe, S.D.; Maslarz, F.; Colt, D.; Cerami,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #authors Wolpe, S.D.; Davatelis, G.; Sherry, B.; Beutler, B.; Hesse, D.G.; Nguyen, H.T.; Moldawer, L.L.; Nathan, C.F.; Lowry, S.F.; Cerami, A.

#journal J. Exp. Med. (1988) 167:570-581
#title Macrophages secrete a novel heparin-binding protein with inflammatory and neutrophil chemokinetic properties.
#accession A27596
##cross-references GB:J04491
NNCE S04533
.thors Davatelis, G.; Tekamp-Olson, P.; Wolpe, S.D.; Hermsen, K.;
Luedke, C.; Gallegos, C.; Coit, D.; Merryweather, J.;
Cerami, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                S.D.; Hermsen, K.;
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J. Immunol. (1991) 146:4031-4040
Genomic structure of murine macrophage inflammatory protein-1-alpha and conservation of potential regulatory sequences with a human homolog, LD78.
                                                                                                                                                                                                                                                                                                                                                                                                A53885
Davatelis, G.; Tekamp-Olson, P.; Wolpe, S.D.; Hermsen, R. Luedke, C.; Gallegos, C.; Coit, D.; Merryweather, J.;
Cerami, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-33,'XX',36-42 ##label WOL
26-Met, 30-Pro, and 39-Thr were also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 1-21,'L',23-61,'A',63-92 ##label BRO
##cross-references GB:M23447
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##molecule_type mRNA
##molecule_type mRNA
##molecule_type mRNA
##molecule_type mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##residues 1-92 ##label DAV ##cross-references EMBL:X12531
                                                                                                                                                                                                      #cross-references MUID:88258380
#accession S04533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type protein
##residues 24-33,''
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type mRNA
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Takao, M.; Hino, J.; Takeshita, N.; Konno, Y.; Nishizawa, T.; Matsuo, H.; Kangawa, K.
Biochem. Biophys. Res. Commun. (1996) 219:656-662
Identification of rat bone morphogenetic protein-3b (BMP-3b), a new member of BMP-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ribosomal protein L7 - slime mold (Dictyostelium discoideum)
#formal_name Dictyostelium discoideum
31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors Szymkowski, D.E.; Kelly, B.; Deering, R.A.
#journal Nucleic Acids Res. (1989) 17:5393
#title A Dictypostellum discoideum cDNA coding for a protein with homology to the rat ribosomal protein L7.
#cross-references MUID:89345108
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#formal_name Rattus norvegicus #common_name Norway rat
10-May-1996 #sequence_revision 19-Jul-1996 #text_change
19-Jul-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 riaknsgtfyvppaakvafvirirgingvspkprkvlkllrllqlnngvfvklnkas 127
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experimental #label MAT
#length 92 #molecular-weight 10345 #checksum 5009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #checksum 1533
                                                                ##cross-references GB:M73061; NID:g199694; CDS_PID:g199695
T This protein is a monokine.
                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.9%; Score 98; DB 6; Length 92; Best Local Similarity 44.4%; Pred. No. 1.51e-01; Matches 12; Conservative 8; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 97; DB 3; Length 246; Pred. No. 2.05e-01; 12; Mismatches 22; Indels
                                                                                                                                                               *superfamily macrophage inflammatory protein heparin binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *Superfamily rat ribosomal protein L7 protein blosynthesis; ribosome #length 246 #molecular-weight 27932
                                                                                                                                                                                                                                             #domain signal sequence #status
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##cross-references EMBL:X14909
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##cross-references DDBJ:D49494
##molecule_type DNA
##wooddines 1-92 ##label RES
                                                                                                                                       23/3; 26/1; 63/2
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Best Local Similarity 36.8%;
Matches 21; Conservative
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#product monocyte chemotactic protein 3 #status
predicted #label MATN
#binding_site carbohydrate (Asn) (covalent) #status
predicted
#length 109 #molecular-weight 12356 #checksum 1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Gaps
  ##residues 1-109 ##label MIN
##cross-references EMBL:X71087
TT This protein induces proteinase secretion and chemotaxis by macrophages and monocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.3%; Score 91; DB 6; Length 109; Best Local Similarity 29.2%; Pred. No. 1.24e+00; Matches 21; Conservative 17; Mismatches 27; Indels
                                                                                                        GENETICS
#gene GDB:SCYA7; SCYA6; MCP-3
##eross-references GDB:138473
#map_position 1741-17412
#introns 36/1; 75/2
CLASSIFICATION #superfamily macrophage inflammatory protein cytokine; glycoprotein; inflammation FEATURE #domain signal sequence #status predicte 1-33
#product monocyte chemotactic protein 3
##residues
                                                         COMMENT
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99 hldkktqt-pkl 109 || : :|| 89 LLDARNKVFAKL 100

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SUMMARIES

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****	[======================================	Release 2 Copyright D	MPsrch_nn n.a Run on: Tabular output	e: Description: Perfect Score: N.A. Sequence: Comp: Scoring table:	Nmatch STD: Searched:	Post-processing	Database:	,		Database:	Statistics

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
Bulte, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Waj, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Finc, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., tae; mitochondrial eukaryotes; Metazoa; Chordata; 18-APR-1997 EST101116 Thymus III
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VD68a11.r1 Barstead m
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Human fetal brain CDN
mx18e02.r1 Soares mou mt04e07.rl Soares mou va94d04.rl Soares mou Human fetal brain cDN vb7ze11.rl Soares mou 291 bp mRNA EST Thymus III Homo sapiens cDNA 5' end. RICC1646B AA176022 RICR2825A AA278864 AA176034 AA260469 AA270895 AA267728 AA396012 AA396012 AA21100 AA21995 AA21995 AA21995 AA21995 C16061 AA40261 AA244918 AA241234 W40015 AA440484 AA271476 AA042856 ALIGNMENTS H 15 110 110 97 47 11 93 8 291 274 274 256 256 444 423 331 413 413 94 Length 259 269 295 349 AUTHORS

JOURNAL MEDLINE

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FEATURES

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NCE Adams, M. D., Kellavage, A. R., Fleischmann, R. D., Fuldner, R. A., Adams, M. D., Kellavage, A. R., Fileischmann, R. D., Fuldner, T. Buth, C., Blake, N. B., Blake, J. B., Brandon, R. C., Man-Wal, C., Sutton, G., Blake, J. B., Brandon, R. C., Man-Wal, C., Clayton, R. A., Cline, T. R., Cotton, M. D. Earle-Hughes, J. Fine, L. D., Filzgerald, L. M., Filzhugh, W. M., Filzhuman, J. L., Geoghagen, N. S., Glodek, A., Gnehm, C. L., Hanna, M. C., Hedblom, E., Hinkle, P. S. Jr., Moreno-Palaques, R. F., McDonald, L. A., Nquyen, D. T., Pelligino, Phillips, C. A., Ryder, S. E., Scott, J. L., Sacudek, D. M., Shiley, R., Small, K. V., Sprigger, T. A., Utterback, T. R., Weidman, J. F., Ld, Y., Bednarik, D. P., Cao, L., Ferrie, A., Coleman, T. A., Collins, E. J., Hw, W. Hu, J. S., Greene, J. M., Gruber, J., Hudson, P., Kim, A. K., Kozak, D. L., Kunsch, C., Hungjun, J., Li, H., Meissner, P. S., Olsen, H., Raymond, L., Weil, Y. F., Wing, J., C., Hungjun, J., Li, H., Meissner, S. W., Dillion, P. J., Fannon, M. R., Rosen, C. A., Haseltine, W. A., Fields, C., Fraser, C. M. and Venter, J. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Initial-assessment-of-human_gene_diversity and expression patterns based upon 83 million nucleotides of-connagemence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423
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Bioinformatics
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               Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Sprigs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dinke, D., Feng, D.F., Ferrie, A., Fischer, C., Hastings, G.A., Rozak, D.L., Kunsch, C., Hudson, P., Kim, A.K., Rozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weisner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Pillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                   Initial assessment of human gene diversity and expression patterns passed upon 83 million nucleotides of CDNA sequence Vature 377 (6547 Suppl), 3-174 (1995)
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For clone availability, additional sequence and expression
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BCORI; Site_2: XhoI"
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Pred. No. 0.00e+00;
0; Mismatches 5; Indels
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Tel: 3018699056
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Best Local Similarity (98.3%;
Matches 286; Conservative
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Email: arkerlav@tigr.org
Spr clone availability, additional sequence and expression
Information related to this EST, please check the TiGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
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                                                                                                                                  /note="Organ: thymus; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
/clone_lib="Thymus III"
/dev_stage="adult"
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalla; Eutherla; Primates; Catarrhini; Hominidae;

Homo sapiens

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By Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man'Wal, C.,

Flizgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,

Glodek, A., Ghehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, F.S.T.,

Kelley, J.G., Kelley, J.C., Liuli, L.I., Marmaros, S.M., Merrick, J.M.,

Phillips, C.A., Kyder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudston, P.S., Olsen, H.,

Kozak, D.L., Kang, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,

Raymond, L., Wei, Y.E., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,

Fraser, C.M. and Venter, J.C.,

Inttal assessment of human gene diversity and expression patterns

AL Nature 377 (6547 Suppl), 3-174 (1995)
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Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TiGR Human Gene
Index (http://www.tigr.org/tdb/hgi/html)
Seq primer: M13 Reverse.
Location/Qualifiers
Location/Qualifiers
1.274
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EcoRI; Site_2: XhoI*
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                                                                                                                          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Contact:-Kerlavage,-AR
Contact:-Kerlavage,-AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Fal: 3018659056
Fax: 3018659423
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Pred. No. 9.84e-300;
0; Mismatches 8;
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                                                                                                                                                                                                                                                                    Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata: Mammalla; Eutherla; Primates; Catarrhini; Hominidae;
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/note="Organ: thymus; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
/clone_lib="Thymus III"
                    18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 aggttttncaaagctccaccacaacacgcagaccttccaagcaggccctcatgctgtaa 120
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9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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                                                end.
AA295945 256 bp mRNA EK
EXT101169 Thymus III Homo sapiens cDNA 5'
91948290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 t
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<1...256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Other_ESTs: THC148619
Contact: Kerlavage, AR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: M13 Reverse.
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Best Local Similarity 97.3%;
Matches 249; Conservative
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l (bases 1 to 231) Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Marra,M., Hillier,L., Allen,M., Le,M., Martin,J., Morris,M., Geisel,S., Kucaba,T., Lacy,M., Tan,F., Underwood,K., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., and Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA270684 231 bp mRNA EST 26-MAR-1997 va69908.r1 Soares mouse 3NME12 5 Mus musculus CDNA clone 736670 5'. AA270684 g1909032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
W444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
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4 GCGGGCATCAGCTCCCTTGACCCAGTGGATATCGGTGGCCCCGTTATTCGTCCAGGTGCC
                                                                                                                                                                                                                                                                                                                                                     /dev_stage="12.5dpc total fetus"
/lab_host="DH10B"
<1..>231
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High quality sequence stop: 186.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
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BASE COUNT
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AUTHORS
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/organism="FVB/N"
/strain="FYB/N"
/note="Vector: pT7T3D-pac (Pharmacia) with a modified
/note="Vector: pT7T3D-pac (Pharmacia) with strand cDNA
/note="Vector: pT7T3D-pac (Pharmacia) polylinker; Site_1: EcoRi; Site_2: NotI; last [5,
was primed with a Not I - oligo(dT) primer [5,
was primed with a Not I and close of representation of grandent construction of grandent construction of grandent of the modified pT7T3 vector:
Library constructed by Bob Barstead."
/clone="762140"
/clone="762140"
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Murinae: Mus.

1 (Bases 1 to 444)

1 (Bases 1 to 444)

Marra,M., Billier,L., Allen,M., E.M., Martin,J., Morris,M., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,G., Morre,B., Schellenber,M., Steptoe,M., Tan,F., Underwood,K., More,B., Schellenber,M., Steptoe,M., Tan,F., Steptoe,M., Tan,F., Wallson,R. and Theising,B., Wille,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R...
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4414 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 316 286 1800
Fax: 316
                                                                                                                                                                                                                                                                                                                                                                                                    AA277792 444 bp mRNA EST .01-APR-1997 vb68all.rl Barstead mouse pooled organs MPLRB4 Mus musculus CDNA clone 762140 5'.
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Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                ö
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Pred. No. 9.48e-114;
O; Mismatches 87; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 403. Location/Qualifiers
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/dev_stage="7 day"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 9
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Query Match
Best Local Similarity 70.2%;
Matches 205; Conservative
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